GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: March 15, 2004, 07:38:19 ; Search time 53 Seconds
(without alignments)
581.088 Million cell updates/sec

Title: US-09-620-955B-4
Perfect score: 109
Sequence: 1 QSALTQPASVSGSPGQSITI.....CSSFANSGPLPGGGTKVTVL 109

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1586107 seqs, 282547505 residues

Word size : 0

Total number of hits satisfying chosen parameters: 916823

Minimum DB seq length: 0
Maximum DB seq length: 109

Post-processing: Listing first 100 summaries

Database : A_Geneseqp_297an04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	109	100.0	109	4	AAB69602	Aab69602 Huntingti
2	28	25.7	90	6	ABJ18698	Abj18698 Antibody
3	28	25.7	95	4	ABG12881	Abg12881 Novel hum
4	28	25.7	95	7	ADE08893	Ade08893 Novel pro
5	26	23.9	104	2	AAB38596	Aar38596 Human lam
6	26	23.9	104	2	AAW58496	Aaw58496 Human lam
7	23	21.1	27	6	ABP56815	Abp56815 Human lam
8	22	20.2	22	5	AAU70414	Aau70414 Human lig
9	22	20.2	94	2	AAR22580	Aar22580 Light cha
10	22	20.2	100	3	AAB01957	Aab01957 Wild-type
11	22	20.2	109	4	AAB01960	Aab01960 High affi
12	21	19.3	92	3	AAB53507	Aab53507 Human col
13	21	19.3	97	4	ABB39374	Abb39374 Peptide #
14	21	19.3	97	4	AAM32889	Aam32889 Peptide #
15	21	19.3	97	4	ABB24161	Abb24161 Protein #
16	21	19.3	97	4	AAM72656	Aam72656 Human bon
17	21	19.3	97	4	AAM60052	Aam60052 Human bra
18	21	19.3	97	4	ABG54353	Abg54353 Human liv
19	21	19.3	97	5	ABG42480	Abg42480 Human pep
20	21	19.3	103	2	AAR22579	Aar22579 Light cha
21	19	17.4	32	5	AAU70416	Aau70416 Human lig
22	19	17.4	103	4	AAB84353	Aab84353 Amino aci
23	19	17.4	108	2	AAR88719	Aar88719 Human ant
24	17	15.6	100	3	AAB01958	Aab01958 Strepativ
25	17	15.6	104	4	AAG93626	Aag93626 Human ant
26	17	15.6	104	6	ABC27433	Abc27433 Anti-Rh(D
27	17	15.6	108	4	AAG93625	Aag93625 Human ant
28	17	15.6	108	6	ABC27432	Abc27432 Anti-Rh(D
29	14	12.8	17	5	AAE17909	Aae17909 T-cell re
30	12	11.0	90	4	AAB48026	Aab48026 Light cha
31	12	11.0	97	5	ABP43164	Abp43164 Human ova
32	12	11.0	99	3	AAB40148	Aab40148 Anti-hIL1
33	12	11.0	99	6	ABP56516	Abp56516 Human ant
34	12	11.0	101	2	AAR38604	Aar38604 NEWM ligh
35	12	11.0	103	2	AAR38605	Aar38605 NEWM ligh
36	12	11.0	103	2	AAR52037	Aar52037 Light cha
37	12	11.0	103	2	AAW21635	Aaw21635 NEWM huma
38	12	11.0	103	2	AAW58484	Aaw58484 Human NEW
39	12	11.0	104	4	AAG93606	Aag93606 Human ant
40	12	11.0	104	6	ABC27413	Abc27413 Anti-Rh(D
41	12	11.0	109	2	AAW15525	Aaw15525 Anti-TGF
42	11	10.1	75	2	AAW62802	Aaw62802 Amino aci
43	11	10.1	75	2	AAW62818	Aaw62818 Amino aci
44	11	10.1	76	2	AAW80980	Aaw80980 Variable
45	11	10.1	76	6	ABC04825	Abc04825 Human epi
46	11	10.1	88	3	AAY56654	Aay56654 Partial p
47	11	10.1	90	4	ABB19441	Abb19441 Protein #
48	11	10.1	90	4	AAM67153	Aam67153 Human bon
49	11	10.1	94	4	AAM54766	Aam54766 Human bra
50	11	10.1	90	4	ABG48819	Abg48819 Human liv
51	11	10.1	90	4	AAM02744	Aam02744 Peptide #
52	11	10.1	90	5	ABJ36817	Abj36817 Human pep
53	11	10.1	92	7	ADC99831	Adc99831 Anti-huma
54	11	10.1	92	7	ADD05435	Add05435 Anti-MUC1
55	11	10.1	95	2	AAR57478	Aar57478 Human K10
56	11	10.1	95	2	AAR92081	Aar92081 Human K10
57	11	10.1	95	5	ABG31428	Abg31428 Amino aci
58	11	10.1	95	6	ABC27123	Abc27123 Human ger
59	11	10.1	95	6	ABC27130	Abc27130 Human ger
60	11	10.1	95	6	ABC27124	Abc27124 Human ger
61	11	10.1	95	6	ABC27131	Abc27131 Human ger
62	11	10.1	95	6	ABC27139	Abc27139 Human ger
63	11	10.1	95	7	ADC99830	Adc99830 Germline
64	11	10.1	95	7	ADD05434	Add05434 Anti-MUC1
65	11	10.1	96	2	AAW58501	Aaw58501 Human lam
66	11	10.1	104	2	AAW62821	Aaw62821 Amino aci
67	11	10.1	105	2	AAR88717	Aar88717 Human ant
68	11	10.1	105	2	AAW80978	Aaw80978 Kappa lig
69	11	10.1	105	2	AAW80968	Aaw80968 Kappa lig
70	11	10.1	105	6	ABB54905	Abb54905 Light cha
71	11	10.1	105	6	ABC04842	Abc04842 Human epi
72	11	10.1	105	6	ABC04831	Abc04831 Human epi
73	11	10.1	106	2	AAR25727	Aar25727 Humanised
74	11	10.1	106	2	AAR90686	Aar90686 Humanized
75	11	10.1	106	4	AAE10473	Aae10473 Humanised
76	11	10.1	106	4	AAE10507	Aae10507 Humanised
77	11	10.1	106	4	AAE10475	Aae10475 Humanised
78	11	10.1	106	4	AAG63262	Aag63262 Anti-RSV
79	11	10.1	106	4	AAG63258	Aag63258 Anti-RSV
80	11	10.1	106	4	AAG63264	Aag63264 Anti-RSV
81	11	10.1	106	4	AAG63266	Aag63266 Anti-RSV
82	11	10.1	106	4	AAG63260	Aag63260 Anti-RSV
83	11	10.1	106	4	AAG63242	Aag63242 Mouse ant
84	11	10.1	106	4	AAB69674	Aab69674 Humanised
85	11	10.1	106	4	AAB69658	Aab69658 Humanised
86	11	10.1	106	5	ABP66375	Abp66375 Human RSV
87	11	10.1	106	5	ABP66406	Abp66406 Human RSV
88	11	10.1	106	5	ABP66418	Abp66418 Human RSV
89	11	10.1	106	5	ABP66392	Abp66392 Human RSV
90	11	10.1	106	5	ABP66403	Abp66403 Human RSV
91	11	10.1	106	5	ABP66388	Abp66388 Human RSV
92	11	10.1	106	5	ABP66400	Abp66400 Human RSV
93	11	10.1	106	5	ABP66424	Abp66424 Human RSV
94	11	10.1	106	5	ABP66430	Abp66430 Human RSV
95	11	10.1	106	5	ABP66362	Abp66362 Human RSV
96	11	10.1	106	5	ABP66367	Abp66367 Human RSV
97	11	10.1	106	5	ABP66416	Abp66416 Human RSV
98	11	10.1	106	5	ABP66419	Abp66419 Human RSV

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  99      11   10.1     106  5  ABP66410                       Abp66410 Human RSV
 100      11   10.1     106  5  ABP66414                       Abp66414 Human RSV

                                ALIGNMENTS

RESULT 1
AAB69602
ID   AAB69602 standard; protein; 109 AA.
XX
AC   AAB69602;
XX
DT   30-APR-2001  (first entry)
XX
DE   Huntingtin minimal sPv binding region #2.
XX
KW   Neurological disorder; Huntington's disease; Alzheimer's disease;
KW   Parkinson's disease; prion disease; frontotemporal dementia;
KW   amyotrophic lateral sclerosis; spinal and bulbar muscular atrophy;
KW   dentatorubal-pallidoluysian atrophy; spinocerebellar ataxia type 1; SCA2;
KW   SCA3; SCA4; SCA5; SCA6; SCA7; protein accumulation; intrabody.
XX
OS   Unidentified.
XX
PN   WO200106989-A2.
XX
PD   01-FEB-2001.
XX
PF   24-JUL-2000; 2000WO-US020131.
XX
PR   27-JUL-1999;   99US-0146047P.
PR   21-JUL-2000; 2000US-00620955.
XX
PA   (HUST/) HUSTON J S.
PA   (MESS/) MESSER A.
PA   (LECE/) LECERF J.
XX
PI   Huston JS,  Messer A,  Lecerf J;
XX
DR   WPI; 2001-182700/18.
DR   N-PSDB; AAF58706.
XX
PT   Inhibiting intracellular polypeptide accumulation, useful for treating
PT   neurological disorders, e.g. Alzheimer's disease, comprises contacting
PT   the polypeptide with a specific intrabody.
XX
PS   Claim 21; Page 94; 108pp; English.
XX
CC   The present invention describes a method for inhibiting the formation of
CC   aggregates of certain proteins, involving contacting the protein with a
CC   binding molecule known as an intrabody. Proteins to be bound include
CC   those associated with neurological disorders, and so the method can be
CC   used in the prevention of diseases such as Alzheimer's, Parkinson's and
CC   Huntington's diseases, prion disease, frontotemporal dementia,
CC   amyotrophic lateral sclerosis, spinal and bulbar muscular atrophy,
CC   dentatorubal-pallidoluysian atrophy, spinocerebellar ataxia type 1
CC   (SCA1), SCA2, SCA3, SCA4, SCA5, SCA6 and SCA7
XX
SQ   Sequence 109 AA;

  Query Match          100.0%;  Score 109;  DB 4;  Length 109;
  Best Local Similarity  100.0%;  Pred. No. 2.6e-59;
  Matches  109;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QSALTQPASVSGSPGQSITISCTGTSSDIGAYNYVSWYQQYPGKAPKLLIYDVSNRPSGI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 QSALTQPASVSGSPGQSITISCTGTSSDIGAYNYVSWYQQYPGKAPKLLIYDVSNRPSGI 60

Qy         61 SNRFSGSKSGDTASLTISGLQAEDEADYYCSSFANSGPLFGGGTKVTVL 109
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SNRFSGSKSGDTASLTISGLQAEDEADYYCSSFANSGPLFGGGTKVTVL 109


RESULT 2
ABJ18698
ID   ABJ18698 standard; protein; 90 AA.
XX
AC   ABJ18698;
XX
DT   06-MAR-2003  (first entry)
XX
DE   Antibody library related human protein sequence SEQ ID No 27.
XX
KW   Library; recombinant antibody; clustering variable region; in silico;
KW   immunogenecity; antibody therapeutic; human.
XX
OS   Homo sapiens.
XX
PN   WO200284277-A1.
XX
PD   24-OCT-2002.
XX
PF   17-APR-2002; 2002WO-US012202.
XX
PR   17-APR-2001; 2001US-0284407P.
XX
PA   (ABMA-) ABMAXIS INC.
XX
PI   Luo P;
XX
DR   WPI; 2003-093043/08.
XX
PT   Constructing a library of recombinant antibodies useful as source of
PT   antibody candidates for screening antigens comprises clustering variable
PT   regions of antibodies having known 3-dimensional structures into
PT   structural ensembles.
XX
PS   Disclosure; Page 116; 119pp; English.
XX
CC   The invention relates to a novel method for the construction of a library
CC   of recombinant antibodies. The novel method comprises clustering variable
CC   regions of a collection of antibodies having known 3D structures into at
CC   least two families of structural ensembles, each comprising at least two
CC   different antibody sequences but with substantially identical main chain
CC   conformations. The method is useful for constructing a library of
CC   artificial antibodies in silico which provides a structurally diverse and
CC   yet functionally more relevant source of antibody candidates which can
CC   then be screened for binding a wide variety of target molecules,
CC   including small molecules, and biomacromolecules such as proteins,
CC   peptides and nucleic acids. The libraries constructed are useful as a
CC   source of antibody candidates for further screening for novel antibodies
CC   with high affinity against a wide range of antigens and having no or
CC   minimum immunogenecity to human subjects treated with antibody
CC   therapeutics. This sequence represents a human peptide region of an
CC   antibody relating to the novel antibody library construction method of
CC   the invention
XX
SQ   Sequence 90 AA;

  Query Match          25.7%;  Score 28;  DB 6;  Length 90;
  Best Local Similarity  100.0%;  Pred. No. 1.3e-19;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QSALTQPASVSGSPGQSITISCTGTSSD 28
              ||||||||||||||||||||||||||||
Db          1 QSALTQPASVSGSPGQSITISCTGTSSD 28


RESULT 3
ABG12681
ID   ABG12681 standard; protein; 95 AA.
XX
AC   ABG12681;
XX
DT   13-FEB-2002  (first entry)
```

```
XX
DE   Novel human diagnostic protein #12872.
XX
KW   Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW   food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS   Homo sapiens.
XX
PN   WO200175067-A2.
XX
PD   11-OCT-2001.
XX
PF   30-MAR-2001; 2001WO-US008631.
XX
PR   31-MAR-2000; 2000US-00540217.
PR   23-AUG-2000; 2000US-00649167.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Drmanac RT,  Liu C,  Tang YT;
XX
DR   WPI; 2001-639362/73.
DR   N-PSDB; AAS77068.
XX
PT   New isolated polynucleotide and encoded polypeptides, useful in
PT   diagnostics, forensics, gene mapping, identification of mutations
PT   responsible for genetic disorders or other traits and to assess
PT   biodiversity.
XX
PS   Claim 20; SEQ ID NO 43240; 103pp; English.
XX
CC   The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC   sequences. (I) is useful as hybridisation probes, polymerase chain
CC   reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC   and in recombinant production of (II). The polynucleotides are also used
CC   in diagnostics as expressed sequence tags for identifying expressed
CC   genes. (I) is useful in gene therapy techniques to restore normal
CC   activity of (II) or to treat disease states involving (II). (II) is
CC   useful for generating antibodies against it, detecting or quantitating a
CC   polypeptide in tissue, as molecular weight markers and as a food
CC   supplement. (II) and its binding partners are useful in medical imaging
CC   of sites expressing (II). (I) and (II) are useful for treating disorders
CC   involving aberrant protein expression or biological activity. The
CC   polypeptide and polynucleotide sequences have spplications in
CC   diagnostics, forensics, gene mapping, identification of mutations
CC   responsible for genetic disorders or other traits to assess biodiversity
CC   and to produce other types of data and products dependent on DNA and
CC   amino acid sequences. AR000010-AR030377 represent novel human diagnostic
CC   amino acid sequences of the invention. Note: The sequence data for this
CC   patent did not appear in the printed specification, but was obtained in
CC   electronic format directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 95 AA;

  Query Match          25.7%;  Score 28;  DB 4;  Length 95;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-19;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QSALTQPASVSGSPGQSITISCTGTSSD 28
              ||||||||||||||||||||||||||||
Db         24 QSALTQPASVSGSPGQSITISCTGTSSD 51


RESULT 4
ADE08993
ID   ADE08993 standard; protein; 95 AA.
XX
AC   ADE08993;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Novel protein-related contig polypeptide sequence #59.
XX
KW   novel gene; novel protein; tissue marker; molecular weight marker;
KW   chromosome marker, genetic disorder; contig.
XX
OS   Unidentified.
XX
PN   WO2003054152-A2.
XX
PD   03-JUL-2003.
XX
PF   10-DEC-2002; 2002WO-US039555.
XX
PR   10-DEC-2001; 2001US-0339739P.
PR   11-DEC-2001; 2001US-0339453P.
PR   14-MAR-2002; 2002US-0365091P.
PR   14-MAR-2002; 2002US-0365384P.
PR   12-APR-2002; 2002US-0372381P.
PR   12-APR-2002; 2002US-0372615P.
PR   22-APR-2002; 2002US-00128558.
PR   24-APR-2002; 2002US-0376045P.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Tang YT,  Asundi V,  Goodrich RW,  Ren F,  Zhang J,  Zhao QA,  Wang J;
PI   Ghosh M,  Xue AJ,  Wehrman T,  Weng G,  Zhou P,  Drmanac RT,  Wang Z;
PI   Ma Y,  Wang D,  Chen R,  Xu C,  Boyle BJ;
XX
DR   WPI; 2003-569235/53.
XX
PT   New polynucleotides, useful for expressing recombinant proteins for
PT   analysis, characterisation or therapeutic use, or as markers for tissues
PT   in which the corresponding protein is preferentially expressed.
XX
PS   Disclosure; SEQ ID NO 2537; 1177pp; English.
XX
CC   The invention comprises the amino acid and coding sequences of novel
CC   proteins. The DNA and protein sequences of the invention are useful as:
CC   markers for tissues in which the corresponding protein is preferentially
CC   expressed; as molecular weight markers on gels; as chromosome markers or
CC   tags; to identify chromosomes or to map related gene positions; and to
CC   compare with endogenous DNA sequences in patients to identify potential
CC   genetic disorders. The present amino acid sequence was used in the
CC   exemplification of the invention.
XX
SQ   Sequence 95 AA;

  Query Match          25.7%;  Score 28;  DB 7;  Length 95;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-19;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QSALTQPASVSGSPGQSITISCTGTSSD 28
              ||||||||||||||||||||||||||||
Db         24 QSALTQPASVSGSPGQSITISCTGTSSD 51


RESULT 5
AAR38596
ID   AAR38596 standard; peptide; 104 AA.
XX
AC   AAR38596;
XX
DT   25-MAR-2003  (revised)
DT   28-OCT-1993  (first entry)
XX
DE   Human lambda light chain subgroup 4 (hL4).
XX
KW   Antibody; variable domain; light; L; heavy; H; consensus; affinity;
KW   antigen; immunogenicity; humanisation; framework.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 1
```

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FT                   /note= "residue conserved in less than 50% of the known
FT                   sequences of hL4"
FT     Misc-difference 32
FT                   /note= "residue conserved in less than 50% of the known
FT                   sequences of hL4"
FT     Misc-difference 87
FT                   /note= "residue conserved in less than 50% of the known
FT                   sequences of hL4"
FT     Misc-difference 89 - 92
FT                   /note= "residues conserved in less than 50% of the known
FT                   sequences of hL4"
FT
XX
PN   WO9311794-A1.
XX
PD   24-JUN-1993.
XX
PF   14-DEC-1992;  92WO-US010906.
XX
PR   13-DEC-1991;  91US-00808464.
XX
PA   (XOMA ) XOMA CORP.
XX
PI   Studnicka GM,  Little RG,  Fishwild DM,  Kohn FR;
XX
DR   WPI; 1993-213827/26.
XX
PT   Antibodies prepn. used for treatment of auto-immune diseases - by
PT   replacement of critical residues to reduce immunogenicity but retain
PT   binding affinity, etc.
XX
PS   Claim 2; Page 96; 160pp; English.
XX
CC   The consensus amino acid sequences for the subgroups of light chains (hK1
CC   - AAR38590, hK4 - hK7, hK2 - GST , hL1 - AAR38591, hL2 - AAR38592, hL3 -
CC   AAR38593 , hL6 - AAR38594, hK4 - AAR38595, hL4 - AAR38596, and hL5 -
CC   AAR38597) and heavy chains (hH3 - AAR38598, hH1 - AAR38599 and hH2 -
CC   AAR38600) of human variable domains may be used to prepare, for example,
CC   a modified mouse antibody variable domain that retains the affinity of
CC   the natural domain for antigen while exhibiting reduced immunogenicity in
CC   humans. Unlike other methods of humanisation, which advocate the
CC   replacement of entire antibody framework regions with those of human
CC   antibodies, this method involves only the introduction of human residues
CC   into those positions not critical for antigen binding. This ensures that
CC   the binding properties of the modified antibody are not diminished.
CC   (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 104 AA;

  Query Match          23.9%;  Score 26;  DB 2;  Length 104;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-17;
  Matches   26;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 SALTQPASVSGSPGQSITISCTGTSS 27
              |||||||||||||||||||||||||||
Db          2 SALTQPASVSGSPGQSITISCTGTSS 27


RESULT 6
AAW58496
ID   AAW58496 standard; protein; 104 AA.
XX
AC   AAW58496;
XX
DT   18-AUG-1998  (first entry)
XX
DE   Human lambda light chain subgroup 2 consensus sequence hL2.
XX
KW   Humanised; human; mouse; CD5; anti-CD5 antibody; immunoglobulin;
KW   depletion; cytotoxic; immunoconjugate; fusion protein; psoriasis;
KW   autoimmune disease; rheumatoid arthritis; type I diabetes.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 1
FT                   /note= "not specified"
FT   Misc-difference 32
FT                   /note= "not specified"
FT   Misc-difference 87
FT                   /note= "not specified"
FT   Misc-difference 89
FT                   /note= "not specified"
FT   Misc-difference 90
FT                   /note= "not specified"
FT   Misc-difference 91
FT                   /note= "not specified"
FT   Misc-difference 92
FT                   /note= "not specified"
XX
PN   US5770196-A.
XX
PD   23-JUN-1998.
XX
PF   07-JUN-1995;  95US-00472788.
XX
PR   13-DEC-1991;  91US-00808464.
PR   14-DEC-1992;  92WO-US010906.
PR   23-JUN-1993;  93US-00082842.
XX
PA   (XOMA ) XOMA CORP.
XX
PI   Studnicka GM;
XX
DR   WPI; 1998-376744/32.
XX
PT   Depletion of CD5-positive cells in vivo - using anti-CD5 antibodies with
PT   humanised variable regions.
XX
PS   Disclosure; Col 55-56; 77pp; English.
XX
CC   A method has been developed of depleting CD5+ cells in an animal. The
CC   method comprises administering a cytotoxic protein containing a modified
CC   immunoglobulin (Ig) variable domain, where the protein is an anti-CD5 Ig
CC   molecule or an immunoconjugate or fusion protein containing an anti-CD5
CC   Ig molecule, and where the modified Ig variable domain comprises at least
CC   one of (a) a modified light chain variable region (see AAW58478 or
CC   AAW58480), and (b) a modified heavy chain variable region (see AAW58479
CC   or AAW58481), where AAW58478 and AAW58479 are humanised forms of the H65
CC   light and heavy chain variable domains with low risk amino acid
CC   substitutions [i.e. low risk of reducing antigen-binding specificity.]
CC   and AAW58480 and AAW58481 are humanised forms of the H65 light and heavy
CC   chain variable domains with moderate risk amino acid substitutions and
CC   are present in humanised H65 antibody he3 (ATCC HB 11206). The method is
CC   useful for treating autoimmune diseases, especially systemic lupus
CC   erythematosus, rheumatoid arthritis, psoriasis or type I diabetes. The
CC   present sequence represents a consensus amino acid sequence for light
CC   chain subgroups of human antibody variable domains, from the present
CC   invention
XX
SQ   Sequence 104 AA;

  Query Match          23.9%;  Score 26;  DB 2;  Length 104;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-17;
  Matches   26;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 SALTQPASVSGSPGQSITISCTGTSS 27
              |||||||||||||||||||||||||||
Db          2 SALTQPASVSGSPGQSITISCTGTSS 27


RESULT 7
ABP56815
ID   ABP56815 standard; protein; 27 AA.
XX
AC   ABP56815;
```

```
XX
DT  01-APR-2003  (first entry)
XX
DE  Human lambda chain 2a2:JH2 amino acid sequence #1.
XX
KW  Focused library; genetic package; antibody; kappa light chain; CDR;
KW  lambda light chain; heavy chain; complementary determining region;
KW  diversity.
XX
OS  Homo sapiens.
OS  Synthetic.
XX
PN  WO200261071-A2.
XX
PD  08-AUG-2002.
XX
PF  18-DEC-2001; 2001WO-US050297.
XX
PR  18-DEC-2000; 2000US-0256380P.
XX
PA  (LADN/) LADNER R C.
XX
PI  Ladner RC;
XX
DR  WPI; 2003-067343/06.
XX
PT  Focused library of vectors or genetic packages for displaying or
PT  expressing diversity of an antibody family, comprise variegated DNA
PT  sequences encoding heavy, kappa or lambda light chain complementary
PT  determining regions.
XX
PS  Disclosure; Page 71-72; 92pp; English.
XX
CC  The present invention describes a focused library of vectors or genetic
CC  packages that display, display and express, or comprise a member of a
CC  diverse family of human antibody related peptides, polypeptides and
CC  proteins and collectively display, display or express, or comprise a
CC  portion of the diversity of the antibody family, the vectors or genetic
CC  packages being characterised by variegated DNA sequences that encode a
CC  heavy chain, kappa or lambda light chain complementary determining region
CC  1 (CDR1), CDR2 or CDR3. The focused library of vectors or genetic
CC  packages of the present invention are useful for displaying, or
CC  displaying and expressing the focused diversity of the family. The
CC  present invention, as compared to prior art, is less time consuming, more
CC  efficient and less cumbersome in the construction of libraries of vectors
CC  and genetic packages using diverse but focused populations of DNA
CC  sequences. ABF56771 to ABP56818 and ABZ22680 to ABZ22747 represent
CC  sequences used in the exemplification of the present invention
XX
SQ  Sequence 27 AA;

  Query Match             21.1%;  Score 23;  DB 6;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 3.9e-15;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QSALTQPASVSGSPGQSITISCT 23
              |||||||||||||||||||||||
Db          3 QSALTQPASVSGSPGQSITISCT 25


RESULT 8
AAU70414
ID  AAU70414 standard; peptide; 22 AA.
XX
AC  AAU70414;
XX
DT  14-FEB-2002  (first entry)
XX
DE  Human light chain immunoglobulin framework region 1 #6.
XX
KW  Immunoglobulin; antibody; light chain; heavy chain; CDR; FR;
KW  complementarity determining region; framework region; IgBP;
KW  transgenic plant; immunoglobulin binding protein array; IgM; IgG; IgA;
KW  IgD; IgE; IgY; IgM; kappa; lambda; CHBP.
XX
OS  Homo sapiens.
XX
PN  WO200183806-A1.
XX
PD  08-NOV-2001.
XX
PF  02-MAY-2001; 2001WO-US014349.
XX
PR  02-MAY-2000; 2000US-00563222.
XX
PA  (EPIC-) EPICYTE PHARM INC.
XX
PI  Hiatt AC,  Hein MB;
XX
DR  WPI; 2002-055482/07.
XX
PT  Preparing immunoglobulin binding protein array in plant cells by
PT  transforming the cells with different polynucleotides encoding binding
PT  protein polypeptides specific to ligand, selecting plant cells for
PT  preparing array.
XX
PS  Disclosure; Fig 1A; 129pp; English.
XX
CC  The invention relates to transforming a population of cells (e.g. plant
CC  cells), comprising using a library of two different polynucleotides
CC  encoding different immunoglobulin binding protein (IgBP) polypeptides
CC  that specifically bind to a ligand or form one or more disulphide bonds
CC  with polypeptides in transfected cells, to generate an IgBP that binds to
CC  a ligand, and transformed plant cells are selected, and preparing an IgBP
CC  array in plant cells. At least one peptide sequence has at least 75%
CC  sequence identity to a framework region (FR) of a native IgM, IgG, IgA,
CC  IgD, IgE, IgY, kappa or lambda immunoglobulin molecule. The method is
CC  useful for preparing an immunoglobulin binding protein array, preferably
CC  heavy chain binding protein (CHBP) array in eukaryotic cells especially
CC  plant cells (e.g. Agrobacterium tumefaciens or maize) or other eukaryotic
CC  cells (e.g. insect cells or mammalian cells). The CHBP is useful for
CC  discovery of e.g. screening assays of IgBPs having desired
CC  characteristics. The present sequence is a mammalian immunoglobulin
CC  derived peptide that may be incorporated into an IgBP of the invention
XX
SQ  Sequence 22 AA;

  Query Match             20.2%;  Score 22;  DB 5;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 3.1e-14;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QSALTQPASVSGSPGQSITISC 22
              ||||||||||||||||||||||
Db          1 QSALTQPASVSGSPGQSITISC 22


RESULT 9
AAR22580
ID  AAR22580 standard; protein; 94 AA.
XX
AC  AAR22580;
XX
DT  21-MAY-1992  (first entry)
XX
DE  Light chain VL16.1 from lysozyme binding scFv fragment.
XX
KW  Fd; bacteriophage; gene III; filamentous; phagemid; capsid; coat; pilus;
KW  g3p; binding; adsorption; gene VIII; diverse repertoire;
KW  specific binding pairs; replicable genetic display package; human.
XX
OS  Homo sapiens.
XX
PN  WO9201047-A.
XX
PD  23-JAN-1992.
XX
```

```
PF   10-JUL-1990;   90GB-00015198.
XX
PR   10-JUL-1990;   90GB-00015198.
PR   19-OCT-1990;   90GB-00022845.
PR   12-NOV-1990;   90GB-00024503.
PR   06-MAR-1991;   91GB-00004744.
PR   15-MAY-1991;   91GB-00010549.
XX
PA   (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
PA   (MEDI-) MED RES COUNCIL.
XX
PI   Mccafferty J,  Pope AR,  Johnson KS,  Hoogenboom HRJ,  Griffiths AD;
PI   Jackson RH,  Holliger KP,  Marks JD;
XX
DR   WPI; 1992-056862/07.
XX
PT   Producing members of specific binding pairs - by expression in
PT   recombinant host cells with a secreting replicable genetic display
PT   package.
XX
PS   Table 11; Page 152; 209pp; English.
XX
CC   PCR was used to prepare a human scFv library from RNA from white blood
CC   cells from an unimmunised donor. Heavy chains from IgG and IgM antibodies
CC   were amplified separately. Four separate libraries were generated (IgG-K,
CC   IgG-lambda, IgM-K and IgM-lambda). The purified scFv fragments were
CC   ligated into the phagemid pHEN1 for expression on the surface of fd
CC   bacteriophage as gene III fusions. The clones were then subjected to
CC   affinity selection for binding to lysozyme by selection on tubes followed
CC   by analysis by ELISA. 50 positive lysozyme binding clones were
CC   identified, >95% being from the IgM library. The clones gave three
CC   different BstNI restriction patterns, and at least 2 clones from each
CC   pattern was sequenced. The sequences indicated the presence of 4 unique
CC   human VH-VL combinations. The sequence shown here is one of the light
CC   chains found. See also AAR21260-307, 309-312, AAR22450, AAR22565,
CC   AAR22567-81
XX
SQ   Sequence 94 AA;

  Query Match             20.2%;  Score 22;  DB 2;  Length 94;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-13;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QSALTQPASVSGSPGQSITISC 22
              ||||||||||||||||||||||
Db          1 QSALTQPASVSGSPGQSITISC 22


RESULT 10
AAB01957
ID   AAB01957 standard; protein; 100 AA.
XX
AC   AAB01957;
XX
DT   18-SEP-2000  (first entry)
XX
DE   Wild-type Ramos cell VL.
XX
KW   Lymphoid cell; antibody producing cell; Ramos cell; immunoglobulin M;
KW   IgM; V gene diversity; directed constitutive hypermutation;
KW   target sequence diversification; terminal deoxynucleotidyl transferase;
KW   TdT; clonal expansion; selection; light chain variable region; VL.
XX
OS   Homo sapiens.
XX
PN   WO2000022111-A1.
XX
PD   20-APR-2000.
XX
PF   08-OCT-1999;   99WO-GB003358.
XX
PR   09-OCT-1998;   98GB-00022104.
PR   19-JAN-1999;   99GB-00001141.
XX
PR   09-JUN-1999;   99GB-00013435.
XX
PA   (MEDI-) MEDICAL RES COUNCIL.
XX
PI   Sale JE,  Neuberger MS,  Cumbers SJ;
XX
DR   WPI; 2000-317971/27.
DR   N-PSDB; AAA52443.
XX
PT   Lymphoid cell line preparation useful for producing gene products having
PT   desired activity, involves screening and selecting cells having ongoing
PT   target sequence diversification and higher mutation rates.
XX
PS   Example 5; Fig 11; 69pp; English.
XX
CC   The invention relates to a method of preparing a lymphoid cell line
CC   capable of capable of directed constitutive hypermutation of a target
CC   nucleic acid region. The method comprises screening a cell population for
CC   ongoing target sequence diversification and selecting a cell in which the
CC   rate of target nucleic acid mutation exceeds that of other nucleic acid
CC   mutation by a factor of 100 or more. The invention also relates to a
CC   method for preparing a gene product with a desired activity, comprising
CC   expressing a nucleic acid encoding the target gene operably linked to a
CC   sequence which directs hypermutation e.g., terminal deoxynucleotidyl
CC   transferase (TdT), in the lymphoid cell line, and identifying a cell or
CC   cells which express a mutated gene product with the desired activity. One
CC   or more clonal populations of the identified cells is established, and
CC   cells with an improved activity of interest are selected. These steps may
CC   be iteratively repeated until a gene product with a desired of activity
CC   is obtained. The cell lines prepared according to the method of the
CC   invention are used for directed constitutive hypermutation of a nucleic
CC   acid region in the preparation of a gene product, preferably an enzyme or
CC   an immunoglobulin, having with a desired activity. In the exemplifications
CC   of the invention, IgM-secreting Ramos cells were selected for use as they
CC   undergo hypermutation during clonal expansion. The present sequence
CC   represents the wild-type Ramos cell light chain variable region (VL)
XX
SQ   Sequence 100 AA;

  Query Match             20.2%;  Score 22;  DB 3;  Length 100;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-13;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 PASVSGSPGQSITISCTGTSSD 28
              ||||||||||||||||||||||
Db          1 PASVSGSPGQSITISCTGTSSD 22


RESULT 11
AAB01960
ID   AAB01960 standard; protein; 100 AA.
XX
AC   AAB01960;
XX
DT   18-SEP-2000  (first entry)
XX
DE   High affinity streptavidin-binding mutant Ramos cell VL.
XX
KW   Lymphoid cell; antibody producing cell; Ramos cell; immunoglobulin M;
KW   IgM; V gene diversity; directed constitutive hypermutation;
KW   target sequence diversification; terminal deoxynucleotidyl transferase;
KW   TdT; clonal expansion; selection; light chain variable region; VL;
KW   streptavidin binding; mutant; mutein.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO2000022111-A1.
XX
PD   20-APR-2000.
XX
PF   08-OCT-1999;   99WO-GB003358.
XX
```

```
PR  09-OCT-1998;   98GB-00022104.
PR  19-JAN-1999;   99GB-00001141.
PR  09-JUN-1999;   99GB-00013435.
XX
PA  (MEDI-) MEDICAL RES COUNCIL.
XX
PI  Sale JE, Neuberger MS, Cumbers SJ;
XX
DR  WPI; 2000-317971/27.
DR  N-PSDB; AAA52446.
XX
PT  Lymphoid cell line preparation useful for producing gene products having
PT  desired activity, involves screening and selecting cells having ongoing
PT  target sequence diversification and higher mutation rates.
XX
PS  Example 5; Fig 16; 69pp; English.
XX
CC  The invention relates to a method of preparing a lymphoid cell line
CC  capable of capable of directed constitutive hypermutation of a target
CC  nucleic acid region. The method comprises screening a cell population for
CC  ongoing target sequence diversification and selecting a cell in which the
CC  rate of target nucleic acid mutation exceeds that of other nucleic acid
CC  mutation by a factor of 100 or more. The invention also relates to a
CC  method for preparing a gene product with a desired activity, comprising
CC  expressing a nucleic acid encoding the target gene operably linked to a
CC  sequence which directs hypermutation e.g., terminal deoxynucleotidyl
CC  transferase (TdT), in the lymphoid cell line, and identifying a cell or
CC  cells which express a mutated gene product with the desired activity. One
CC  or more clonal populations of the identified cells is established, and
CC  cells with an improved activity of interest are selected. These steps may
CC  be iteratively repeated until a gene product with a desired of activity
CC  is obtained. The cell lines prepared according to the method of the
CC  invention are used for directed constitutive hypermutation of a nucleic
CC  acid region in the preparation of a gene product, preferably an enzyme or
CC  an immunoglobulin (Ig) with a desired activity. In the exemplifications
CC  of the invention, IgM-secreting Ramos cells were selected for use as they
CC  undergo hypermutation during clonal expansion. The present sequence
CC  represents a mutant IgM light chain variable region (VL) from a Ramos
CC  cell which binds streptavidin with high affinity. The cell is the product
CC  of 6 rounds of clonal expansion, hypermutation and selection
XX
SQ  Sequence 100 AA;

  Query Match          20.2%;  Score 22;  DB 3;  Length 100;
  Best Local Similarity  100.0%;  Pred. No. 1.2e-13;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 PASVSGSPGQSITTISCTGTSSD 28
              |||||||||||||||||||||||
Db          1 PASVSGSPGQSITTISCTGTSSD 22


RESULT 12
AAB53507
ID  AAB53507 standard; protein; 92 AA.
XX
AC  AAB53507;
XX
DT  09-MAR-2001  (first entry)
XX
DE  Human colon cancer antigen protein sequence SEQ ID NO:1047.
XX
KW  Human; colon cancer; colon cancer antigen; diagnosis; detection;
KW  identification; cytostatic; cardioactive; neuroprotective; vulnerary;
KW  immunomodulatory; muscular; gynaecological; gastrointestinal;
KW  nephrotropic; antiinfective; antibacterial; gene therapy; wound;
KW  neural disorder; immune system disorder; muscular disorder;
KW  reproductive disorder; gastrointestinal disorder; renal disorder;
KW  infectious disease; cardiovascular disorder.
XX
OS  Homo sapiens.
XX
PN  WO200055351-A1.
XX
PD  21-SEP-2000.
XX
PF  08-MAR-2000; 2000WO-US005883.
XX
PR  12-MAR-1999;   99US-0124270P.
XX
PA  (HUMA-) HUMAN GENOME SCI INC.
XX
PI  Rosen CA, Ruben SM;
XX
DR  WPI; 2000-587534/55.
DR  N-PSDB; AAC98264.
XX
PT  Colon cancer associated gene sequences, referred to as colon cancer
PT  antigens, useful for the treatment, prevention, and diagnosis of colon
PT  disorders such as colon cancer.
XX
PS  Claim 11; Page 1627-1628; 2104pp; English.
XX
CC  AAC97991 to AAC98763 encode the human colon cancer associated proteins,
CC  called human colon cancer antigens, given in AAB53234 to AAB54006. The
CC  human colon cancer antigens can have cytostatic, cardioactive, muscular;
CC  neuroprotective, immunomodulatory, gynaecological, gastrointestinal,
CC  vulnerary, nephrotropic, antiinfective and antibacterial activities, and
CC  can be used in gene therapy. The colon cancer antigen polynucleotides,
CC  proteins and antibodies to the proteins are useful for the prevention,
CC  treatment and diagnosis of colon disorders, such as colon cancer. The
CC  polynucleotides may be used in diagnostics and research, such as for
CC  chromosome identification, and as hybridisation probes. The proteins may
CC  also be used to prevent diseases such as neural disorders, immune system
CC  disorders, muscular disorders, reproductive disorders, gastrointestinal
CC  disorders, wounds, renal disorders, infectious diseases, and
CC  cardiovascular disorders. AAC98764 to AAC98772 represent
CC  sequences used in the exemplification of the present invention
XX
SQ  Sequence 92 AA;

  Query Match          19.3%;  Score 21;  DB 3;  Length 92;
  Best Local Similarity  100.0%;  Pred. No. 5.1e-12;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         72 TASLTISGLQAEDEADYYCSS 92
              |||||||||||||||||||||
Db         11 TASLTISGLQAEDEADYYCSS 31


RESULT 13
ABB39374
ID  ABB39374 standard; peptide; 97 AA.
XX
AC  ABB39374;
XX
DT  04-FEB-2002  (first entry)
XX
DE  Peptide #6880 encoded by human foetal liver single exon probe.
XX
KW  Human; foetal liver; gene expression; single exon nucleic acid probe.
XX
OS  Homo sapiens.
XX
PN  WO200157277-A2.
XX
PD  09-AUG-2001.
XX
PF  30-JAN-2001; 2001WO-US000669.
XX
PR  04-FEB-2000; 2000US-0180312P.
PR  26-MAY-2000; 2000US-0207456P.
PR  30-JUN-2000; 2000US-0060840S.
PR  03-AUG-2000; 2000US-0063266.
PR  21-SEP-2000; 2000US-0234687P.
PR  27-SEP-2000; 2000US-0236359P.
```

```
PR  04-OCT-2000; 2000GB-00024263.
XX
PA  (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI  Penn SG,  Hanzel DK,  Chen W,  Rank DR;
XX
DR  WPI; 2001-483447/52.
XX
PT  Human genome-derived single exon nucleic acid probes useful for analyzing
PT  gene expression in human fetal liver.
XX
PS  Claim 27; SEQ ID NO 32009; 639pp + Sequence Listing; English.
XX
CC  The invention relates to a single exon nucleic acid probe for measuring
CC  human gene expression in a sample derived from human foetal liver. The
CC  single exon nucleic acid probes may be used for predicting, measuring and
CC  displaying gene expression in samples derived from human fetal liver. The
CC  present sequence is a peptide encoded by a single exon nucleic acid probe
CC  of the invention. Note: The sequence data for this patent did not form
CC  part of the printed specification, but was obtained in electronic format
CC  directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ  Sequence 97 AA;

  Query Match           19.3%;  Score 21;  DB 4;  Length 97;
  Best Local Similarity  100.0%;  Pred. No. 1.1e-12;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 ASVSGSPQQSITISCTGTSSD 28
              |||||||||||||||||||||
Db          1 ASVSGSPQQSITISCTGTSSD 21


RESULT 14
AAM32889
ID  AAM32889 standard; protein; 97 AA.
XX
AC  AAM32889;
XX
DT  17-OCT-2001  (first entry)
XX
DE  Peptide #6926 encoded by probe for measuring placental gene expression.
XX
KW  Probe; microarray; human; placenta; antenatal diagnosis;
KW  genetic disorder.
XX
OS  Homo sapiens.
XX
PN  WO200157272-A2.
XX
PD  09-AUG-2001.
XX
PF  30-JAN-2001; 2001WO-US000663.
XX
PR  04-FEB-2000; 2000US-0180312P.
PR  26-MAY-2000; 2000US-0207456P.
PR  30-JUN-2000; 2000US-00608408.
PR  03-AUG-2000; 2000US-00632366.
PR  21-SEP-2000; 2000US-0234687P.
PR  27-SEP-2000; 2000US-0236359P.
PR  04-OCT-2000; 2000GB-00024263.
XX
PA  (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI  Penn SG,  Hanzel DK,  Chen W,  Rank DR;
XX
DR  WPI; 2001-488897/53.
XX
PT  Human genome-derived single exon nucleic acid probes useful for analyzing
PT  gene expression in human placenta.
XX
PS  Claim 27; SEQ ID NO 33158; 654pp; English.
XX
CC  The present invention relates to single exon nucleic acid probes (SENP;
CC  see AAI31315-AAI57546). The present sequence is a peptide encoded by one
CC  such probe. The probes are useful for producing a microarray for
CC  predicting, measuring and displaying gene expression in samples derived
CC  from human placenta. The probes are useful for antenatal diagnosis of
CC  human genetic disorders
XX
SQ  Sequence 97 AA;

  Query Match           19.3%;  Score 21;  DB 4;  Length 97;
  Best Local Similarity  100.0%;  Pred. No. 1.1e-12;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 ASVSGSPQQSITISCTGTSSD 28
              |||||||||||||||||||||
Db          1 ASVSGSPQQSITISCTGTSSD 21


RESULT 15
ABB24161
ID  ABB24161 standard; protein; 97 AA.
XX
AC  ABB24161;
XX
DT  23-JAN-2002  (first entry)
XX
DE  Protein #6160 encoded by probe for measuring heart cell gene expression.
XX
KW  Human; gene expression; heart; microarray; vascular system;
KW  cardiovascular disease; hypertension; cardiac arrhythmia;
KW  congenital heart disease.
XX
OS  Homo sapiens.
XX
PN  WO200157274-A2.
XX
PD  09-AUG-2001.
XX
PF  30-JAN-2001; 2001WO-US000666.
XX
PR  04-FEB-2000; 2000US-0180312P.
PR  26-MAY-2000; 2000US-0207456P.
PR  30-JUN-2000; 2000US-00608408.
PR  03-AUG-2000; 2000US-00632366.
PR  21-SEP-2000; 2000US-0234687P.
PR  27-SEP-2000; 2000US-0236359P.
PR  04-OCT-2000; 2000GB-00024263.
XX
PA  (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI  Penn SG,  Hanzel DK,  Chen W,  Rank DR;
XX
DR  WPI; 2001-488899/53.
XX
PT  Single exon nucleic acid probes for analyzing gene expression in human
PT  hearts.
XX
PS  Claim 15; SEQ ID NO 25931; 530pp; English.
XX
CC  The present invention relates to single exon nucleic acid probes for
CC  measuring human gene expression in a sample derived from human heart (see
CC  ABA21535-ABA41305). The present sequence is a protein encoded by one such
CC  probe. The probes may be used for predicting, measuring and displaying
CC  gene expression in samples derived from the human heart via microarrays.
CC  By measuring gene expression, the probes are useful for predicting,
CC  diagnosing, grading, staging, monitoring and prognosing diseases of the
CC  human heart and vascular system e.g. cardiovascular disease,
CC  hypertension, cardiac arrhythmias and congenital heart disease. Note: The
CC  sequence data for this patent did not form part of the printed
CC  specification, but was obtained in electronic format directly from WIPO
CC  at ftp.wipo.int/pub/published_pct_sequences
XX
SQ  Sequence 97 AA;
```

```
  Query Match             19.3%;  Score 21;  DB 4;  Length 97;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-12;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 ASVSGSPGQSITISCTGTSSD 28
              |||||||||||||||||||||
Db          1 ASVSGSPGQSITISCTGTSSD 21


RESULT 16
AAM72656
ID   AAM72656 standard; protein; 97 AA.
XX
AC   AAM72656;
XX
DT   06-NOV-2001  (first entry)
XX
DE   Human bone marrow expressed probe encoded protein SEQ ID NO: 32962.
XX
KW   Human; bone marrow expressed exon; gene expression analysis; probe;
KW   microarray; cancer; leukaemia; lymphoma; myeloma.
XX
OS   Homo sapiens.
XX
PN   WO200157276-A2.
XX
PD   09-AUG-2001.
XX
PF   30-JAN-2001; 2001WO-US000668.
XX
PR   04-FEB-2000; 2000US-0180312P.
PR   26-MAY-2000; 2000US-0207456P.
PR   30-JUN-2000; 2000US-00608408.
PR   03-AUG-2000; 2000US-00632366.
PR   21-SEP-2000; 2000US-0234687P.
PR   27-SEP-2000; 2000US-0236359P.
PR   04-OCT-2000; 2000GB-00024263.
XX
PA   (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI   Penn SG,  Hanzel DK,  Chen W,  Rank DR;
XX
DR   WPI; 2001-488900/53.
XX
PT   Human genome-derived single exon nucleic acid probes useful for analyzing
PT   gene expression in human bone marrow.
XX
PS   Example 4; SEQ ID NO 32962; 658pp + Sequence Listing; English.
XX
CC   The present invention provides a number of single exon nucleic acid
CC   probes which are derived from genomic sequences expressed in the human
CC   bone marrow. They can be used to measure gene expression in bone marrow
CC   samples, which may enable the improved diagnosis and treatment of cancers
CC   such as lymphoma, leukaemia and myeloma. The present sequence is a
CC   protein encoded by one of the probes of the invention
XX
SQ   Sequence 97 AA;

  Query Match             19.3%;  Score 21;  DB 4;  Length 97;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-12;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 ASVSGSPGQSITISCTGTSSD 28
              |||||||||||||||||||||
Db          1 ASVSGSPGQSITISCTGTSSD 21


RESULT 17
AAM60052
ID   AAM60052 standard; protein; 97 AA.
XX
AC   AAM60052;
XX
DT   05-NOV-2001  (first entry)
XX
DE   Human brain expressed single exon probe encoded protein SEQ ID NO: 32157.
XX
KW   Human; brain expressed exon; gene expression analysis; probe; microarray;
KW   Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.
XX
OS   Homo sapiens.
XX
PN   WO200157275-A2.
XX
PD   09-AUG-2001.
XX
PF   30-JAN-2001; 2001WO-US000667.
XX
PR   04-FEB-2000; 2000US-0180312P.
PR   26-MAY-2000; 2000US-0207456P.
PR   30-JUN-2000; 2000US-00608408.
PR   03-AUG-2000; 2000US-00632366.
PR   21-SEP-2000; 2000US-0234687P.
PR   27-SEP-2000; 2000US-0236359P.
PR   04-OCT-2000; 2000GB-00024263.
XX
PA   (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI   Penn SG,  Hanzel DK,  Chen W,  Rank DR;
XX
DR   WPI; 2001-483446/52.
XX
PT   Single exon nucleic acid probes for analyzing gene expression in human
PT   brains.
XX
PS   Example 4; SEQ ID NO 32157; 650pp + Sequence Listing; English.
XX
CC   The present invention provides a number of single exon nucleic acid
CC   probes which are derived from genomic sequences expressed in the human
CC   brain. They can be used to measure gene expression in brain cell samples,
CC   which may enable the diagnosis and improved treatment of nervous system
CC   diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
CC   epilepsy and cancers. The present sequence is a protein encoded by one of
CC   the probes of the invention
XX
SQ   Sequence 97 AA;

  Query Match             19.3%;  Score 21;  DB 4;  Length 97;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-12;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 ASVSGSPGQSITISCTGTSSD 28
              |||||||||||||||||||||
Db          1 ASVSGSPGQSITISCTGTSSD 21


RESULT 18
ABG54353
ID   ABG54353 standard; peptide; 97 AA.
XX
AC   ABG54353;
XX
DT   25-FEB-2003  (first entry)
XX
DE   Human liver peptide, SEQ ID No 33001.
XX
KW   Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;
KW   hypercholesterolaemia; coronary heart disease.
XX
OS   Homo sapiens.
XX
PN   WO200157273-A2.
XX
PD   09-AUG-2001.
XX
```

```
PF   30-JAN-2001; 2001WO-US000664.
XX
PR   04-FEB-2000; 2000US-0180312P.
PR   26-MAY-2000; 2000US-0207456P.
PR   30-JUN-2000; 2000US-0060840S.
PR   03-AUG-2000; 2000US-0063236S.
PR   21-SEP-2000; 2000US-0234687P.
PR   27-SEP-2000; 2000US-0236359P.
PR   04-OCT-2000; 2000GB-0024263.
XX
PA   (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI   Penn SG,  Hanzel DK,  Chen W,  Rank DR;
XX
DR   WPI; 2001-488898/53.
XX
PT   Human genome-derived single exon nucleic acid probes useful for analyzing
PT   gene expression in human adult liver.
XX
PS   Claim 27; SEQ ID NO 33001; 658pp; English.
XX
CC   The invention relates to a single exon nucleic acid probe (SENP) (I) for
CC   measuring human gene expression in a sample derived from human adult
CC   liver, comprising one of 13109 defined nucleotide sequences given in the
CC   specification (or complements/ fragments). The probe hybridises at high
CC   stringency to a nucleic acid molecule expressed in the human adult liver.
CC   (I) may be used for predicting, measuring and displaying gene expression
CC   in samples derived from human adult liver. The genes identified may be
CC   involved in genetic liver diseases such as cirrhosis,
CC   hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is
CC   associated with coronary heart disease. ABG47348-ABG59930 represent human
CC   liver single exon encoded peptides of the invention. Note: The sequence
CC   information for this patent does not appear in the printed specification
CC   but was obtained in electronic format directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 97 AA;

  Query Match          19.3%;  Score 21;  DB 4;  Length 97;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-12;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 ASVSGSPGQSITISCTGTSSD 28
              |||||||||||||||||||||
Db          1 ASVSGSPGQSITISCTGTSSD 21


RESULT 19
ABG42480
ID   ABG42480 standard; peptide; 97 AA.
XX
AC   ABG42480;
XX
DT   19-AUG-2002  (first entry)
XX
DE   Human peptide encoded by genome-derived single exon probe SEQ ID 32145.
XX
KW   Human; single exon probe; asthma; lung cancer; COPD; ILD;
KW   chronic obstructive pulmonary disease; interstitial lung disease;
KW   familial idiopathic pulmonary fibrosis; neurofibromatosis;
KW   tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
KW   Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
KW   pulmonary histiocytosis; lymphangioleiomyomatosis; Karagener syndrome;
KW   pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
KW   primary ciliary dyskinesia; pulmonary hypertension;
KW   hyaline membrane disease.
XX
OS   Homo sapiens.
XX
PN   WO200186003-A2.
XX
PD   15-NOV-2001.
XX
```

```
PF   30-JAN-2001; 2001WO-US000665.
XX
PR   04-FEB-2000; 2000US-0180312P.
PR   26-MAY-2000; 2000US-0207456P.
PR   30-JUN-2000; 2000US-0060840S.
PR   03-AUG-2000; 2000US-0063236S.
PR   21-SEP-2000; 2000US-0234687P.
PR   27-SEP-2000; 2000US-0236359P.
PR   04-OCT-2000; 2000GB-0024263.
XX
PA   (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI   Penn SG,  Hanzel DK,  Chen W,  Rank DR;
XX
DR   WPI; 2002-114183/15.
XX
PT   Spatially-addressable set of single exon nucleic acid probes, used to
PT   measure gene expression in human lung samples.
XX
PS   Claim 27; SEQ ID NO 32145; 634pp; English.
XX
CC   The invention relates to a spatially-addressable set of single exon
CC   nucleic acid probes for measuring gene expression in a sample derived
CC   from human lung comprising single exon nucleic acid probes having one of
CC   12614 nucleic acid sequences mentioned in the specification, or their
CC   complements or the 12387 open reading frames derived from the 12614
CC   probes. Also included are a microarray comprising the novel set of probes
CC   ; the novel set of probes which hybridise at high stringency to a nucleic
CC   acid expressed in the human lung; measuring gene expression in a sample
CC   derived from human lung, comprising (a) contacting the array with a
CC   collection of detectably labeled nucleic acids derived from human lung
CC   mRNA, and (b) measuring the label detectably bound to each probe of the
CC   array; identifying exons in a eukaryotic genome, comprising (a)
CC   algorithmically predicting at least one exon from genomic sequences of
CC   the eukaryote; and (b) detecting specific hybridisation of detectably
CC   labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
CC   having a fragment identical to the predicted exon, the probe is included
CC   in the above mentioned microarray; assigning exons to a single gene,
CC   comprising (a) identifying exons from genomic sequence by the method
CC   above and (b) measuring the expression of each of the exons in several
CC   tissues and/or cell types using hybridisation to a single exon
CC   microarrays having a probe with the exon, where a common pattern of
CC   expression of the exons in the tissues and/or cell types indicates that
CC   the exons should be assigned to a single gene; a peptide comprising one
CC   of 12011 sequences, mentioned in the specification, or encoded by the
CC   probes open reading frames (ORF). The probes are used for gene expression
CC   analysis, and for identifying exons in a gene, particularly using human
CC   lung derived mRNA and for the study of lung diseases such as asthma, lung
CC   cancer, chronic obstructive pulmonary disease (COPD), interstitial lung
CC   disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,
CC   tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-
CC   Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary
CC   histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis,
CC   Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary
CC   dyskinesia, pulmonary hypertension and hyaline membrane disease. The
CC   present sequence is a peptide/protein encoded by a single exon probe of
CC   the invention. Note: The sequence data for this patent did not form part
CC   of the printed specification, but was obtained in electronic format
CC   directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 97 AA;

  Query Match          19.3%;  Score 21;  DB 5;  Length 97;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-12;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 ASVSGSPGQSITISCTGTSSD 28
              |||||||||||||||||||||
Db          1 ASVSGSPGQSITISCTGTSSD 21


RESULT 20
AAR22579
```

```
ID   AAR22579 standard; protein; 103 AA.
XX
AC   AAR22579;
XX
DT   21-MAY-1992  (first entry)
XX
DE   Light chain VL13.1 from lysozyme binding scFv fragment.
XX
KW   Fd; bacteriophage; gene III; filamentous; phagemid; capsid; coat; pilus;
KW   g3p; binding; adsorption; gene VIII; diverse repertoire;
KW   specific binding pairs; replicable genetic display package; human.
XX
OS   Homo sapiens.
XX
PN   WO9201047-A.
XX
PD   23-JAN-1992.
XX
PF   10-JUL-1990;    90GB-00015198.
XX
PR   10-JUL-1990;    90GB-00015198.
PR   19-OCT-1990;    90GB-00022845.
PR   12-NOV-1990;    90GB-00024503.
PR   06-MAR-1991;    91GB-00004744.
PR   15-MAY-1991;    91GB-00010549.
XX
PA   (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
PA   (MEDI-) MED RES COUNCIL.
XX
PI   Mccafferty J,  Pope AR,  Johnson KS,  Hoogenboom HRJ,  Griffiths AD;
PI   Jackson RH,  Holliger KP,  Marks JD;
XX
DR   WPI; 1992-056862/07.
XX
PT   Producing members of specific binding pairs - by expression in
PT   recombinant host cells with a secreting replicable genetic display
PT   package.
XX
PS   Table 11; Page 152; 209pp; English.
XX
CC   PCR was used to prepare a human scFv library from RNA from white blood
CC   cells from an unimmunised donor. Heavy chains from IgG and IgM antibodies
CC   were amplified separately. Four separate libraries were generated (IgG-K,
CC   IgG-lambda, IgM-K and IgM-lambda). The purified scFv fragments were
CC   ligated into the phagemid pHEN1 for expression on the surface of fd
CC   bacteriophage as gene III fusions. The clones were then subjected to
CC   affinity selection for binding to lysozyme by selection on tubes followed
CC   by analysis by ELISA. 50 positive lysozyme binding clones were
CC   identified, >95% being from the IgM library. The clones gave three
CC   different BstNI restriction patterns, and at least 2 clones from each
CC   pattern was sequenced. The sequences indicated the presence of 4 unique
CC   human VH-VL combinations. The sequence shown here is one of the light
CC   chains found. See also AAR21260-307, 309-312, AAR22450, AAR22565,
CC   AAR22567-81
XX
SQ   Sequence 103 AA;

  Query Match          19.3%;  Score 21;  DB 2;  Length 103;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-12;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 LTGPASVSGSPGQSITISCTG 24
              |||||||||||||||||||||
Db          4 LTGPASVSGSPGQSITISCTG 24


RESULT 21
AAU70416
ID   AAU70416 standard; peptide; 32 AA.
XX
AC   AAU70416;
XX
DT   14-FEB-2002  (first entry)
XX
DE   Human light chain immunoglobulin framework region 3 #6.
XX
KW   Immunoglobulin; antibody; light chain; heavy chain; CDR; FR;
KW   complementarity determining region; framework region; IgBP;
KW   transgenic plant; immunoglobulin binding protein array; IgM; IgG; IgA;
KW   IgD; IgE; IgY; IgM; kappa; lambda; CHBP.
XX
OS   Homo sapiens.
XX
PN   WO200183806-A1.
XX
PD   08-NOV-2001.
XX
PF   02-MAY-2001; 2001WO-US014349.
XX
PR   02-MAY-2000; 2000US-00563222.
XX
PA   (EPIC-) EPICYTE PHARM INC.
XX
PI   Hiatt AC,  Hein MB;
XX
DR   WPI; 2002-055482/07.
XX
PT   Preparing immunoglobulin binding protein array in plant cells by
PT   transforming the cells with different polynucleotides encoding binding
PT   protein polypeptides specific to ligand, selecting plant cells for
PT   preparing array.
XX
PS   Disclosure; Fig 1A; 129pp; English.
XX
CC   The invention relates to transforming a population of cells (e.g. plant
CC   cells), comprising using a library of two different polynucleotides
CC   encoding different immunoglobulin binding protein (IgBP) polypeptides
CC   that specifically bind to a ligand or form one or more disulphide bonds
CC   with polypeptides in transfected cells, to generate an IgBP that binds to
CC   a ligand, and transformed plant cells are selected; and preparing an IgBP
CC   array in plant cells. At least one peptide sequence has at least 75%
CC   sequence identity to a framework region (FR) of a native IgM, IgG, IgA,
CC   IgD, IgE, IgY, kappa or lambda immunoglobulin molecule. The method is
CC   useful for preparing an immunoglobulin binding protein array, preferably
CC   heavy chain binding protein (CHBP) array in eukaryotic cells especially
CC   plant cells (e.g. Agrobacterium tumefaciens or maize) or other eukaryotic
CC   cells (e.g. insect cells or mammalian cells). The CHBP is useful for
CC   discovery of e.g. screening assays of IgBPs having desired
CC   characteristics. The present sequence is a mammalian immunoglobulin
CC   derived peptide that may be incorporated into an IgBP of the invention
XX
SQ   Sequence 32 AA;

  Query Match          17.4%;  Score 19;  DB 5;  Length 32;
  Best Local Similarity   100.0%;  Pred. No. 3.9e-11;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         72 TASLTISGLQAEDEADYYC 90
              |||||||||||||||||||
Db         14 TASLTISGLQAEDEADYYC 32


RESULT 22
AAB84353
ID   AAB84353 standard; protein; 103 AA.
XX
AC   AAB84353;
XX
DT   22-AUG-2001  (first entry)
XX
DE   Amino acid sequence of light chain of intrabody ST6/34.
XX
KW   Surface receptor-dependent infection; pathogenic agent; antibody;
KW   intrabody; ST6/34; chemokine receptor; CCR5.
XX
OS   Oryctolagus cuniculus.
```

XX
PN WO200142308-A2.
XX
PD 14-JUN-2001.
XX
PF 08-DEC-2000; 2000WO-EP012419.
XX
PR 08-DEC-1999; 99US-0169653P.
XX
PA (NOVS) NOVARTIS AG.
PA (SCRI) SCRIPPS RES INST.
XX
PI Barbas CF, Steinberger P;
XX
DR WPI; 2001-381649/40.
XX
PT Inhibiting, preventing or treating pathogenic infection of cells
PT comprises expressing recombinant antibody specific for surface receptor
PT of cells necessary for pathogenic infection, fused to intracellular
PT anchor means.
XX
PS Claim 1; Page 58; 69pp; English.
XX
CC The specification describes a method for inhibiting, diminishing,
CC preventing or treating surface receptor-dependent infection of cells by
CC pathogenic agents. The method comprises a recombinant antibody protein
CC fused to an intracellular anchor means, where the antibody is specific
CC for a surface receptor of the cells necessary for pathogenic infection.
CC The anchor means may be an endoplasmic reticulum retention peptide. The
CC present sequence represents the light chain of the intrabody ST6/34,
CC which is specific for the chemokine receptor CCR5. The present protein is
CC used to produce antibody proteins of the invention
XX
SQ Sequence 103 AA;

Query Match 17.4%; Score 19; DB 4; Length 103;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 72 TASLTISGLQAEDEADYYC 90
||||||||||||||||||||
Db 69 TASLTISGLQAEDEADYYC 87

RESULT 23
AAR88719
ID AAR88719 standard; protein; 108 AA.
XX
AC AAR88719;
XX
DT 26-SEP-1996 (first entry)
XX
DE Human antibody lambda chain variable region consensus sequence.
XX
KW Antibody; stability; instability; mutagenesis; amino acid frequency;
KW canonical sequence approximation; substitution; immunoglobulin;
KW light chain; variable region; VL-region; diagnosis; immunoassay;
KW cancer treatment; autoimmune disease; immunotoxin; improved yield.
XX
OS Homo sapiens.
XX
PN DE4425115-A1.
XX
PD 18-JAN-1996.
XX
PF 15-JUL-1994; 94DE-04425115.
XX
PR 15-JUL-1994; 94DE-04425115.
XX
PA (BOEF) BOEHRINGER MANNHEIM GMBH.
XX
PI Steipe B, Steinbacher S;
XX
DR WPI; 1996-069594/08.
XX
PT Functional antibodies modified to increase or decrease stability - have
PT specific amino acid substns. in the variable domain, determined by
PT reference to consensus sequences.
XX
PS Claim 2; Page 31; 43pp; German.
XX
CC Consensus sequences were established for antibody variable regions from
CC human and mouse heavy and light (kappa and lambda) chains. In addition,
CC frequency tables listing the amino acids which can be found at each
CC position were compiled. In a new method, mutations are introduced into an
CC antibody variable domain by reference to the frequency table. When an
CC amino acid is replaced by one which occurs at a higher frequency at that
CC posn. the resulting antibody chain is more stable than the wild-type;
CC when an amino acid is replaced by one which occurs less frequently (or
CC not at all), the resulting antibody is less stable than the wild-type.
CC Stabilised antibodies are useful as diagnostic reagents, as catalysts and
CC in treatment of cancer, autoimmune diseases and infections. Destabilised
CC antibodies have improved (faster) pharmacokinetic properties. The present
CC sequence is the human lambda light chain variable region consensus
CC sequence
XX
SQ Sequence 108 AA;

Query Match 17.4%; Score 19; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 72 TASLTISGLQAEDEADYYC 90
||||||||||||||||||||
Db 69 TASLTISGLQAEDEADYYC 87

RESULT 24
AAB01958
ID AAB01958 standard; protein; 100 AA.
XX
AC AAB01958;
XX
DT 18-SEP-2000 (first entry)
XX
DE Strepatividin-binding mutant Ramos cell VL.
XX
KW Lymphoid cell; antibody producing cell; Ramos cell; immunoglobulin M;
KW IgM; V gene diversity; directed constitutive hypermutation;
KW target sequence diversification; terminal deoxynucleotidyl transferase;
KW TdT; clonal expansion; selection; light chain variable region; VL;
KW streptavidin binding; mutant; mutein.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200022111-A1.
XX
PD 20-APR-2000.
XX
PF 08-OCT-1999; 99WO-GB003358.
XX
PR 09-OCT-1998; 98GB-00022104.
PR 19-JAN-1999; 99GB-00001141.
PR 09-JUN-1999; 99GB-00013435.
XX
PA (MEDI-) MEDICAL RES COUNCIL.
XX
PI Sale JE, Neuberger MS, Cumbers SJ;
XX
DR WPI; 2000-317971/27.
DR N-PSDB; AAA52444.
XX
PT Lymphoid cell line preparation useful for producing gene products having
PT desired activity, involves screening and selecting cells having ongoing
PT target sequence diversification and higher mutation rates.

XX
PS Example 5; Fig 11; 69pp; English.
XX
CC The invention relates to a method of preparing a lymphoid cell line
CC capable of capable of directed constitutive hypermutation of a target
CC nucleic acid region. The method comprises screening a cell population for
CC ongoing target sequence diversification and selecting a cell in which the
CC rate of target nucleic acid mutation exceeds that of other nucleic acid
CC mutation by a factor of 100 or more. The invention also relates to a
CC method for preparing a gene product with a desired activity, comprising
CC expressing a nucleic acid encoding the target gene operably linked to a
CC sequence which directs hypermutation e.g., terminal deoxynucleotidyl
CC transferase (TdT), in the lymphoid cell line, and identifying a cell or
CC cells which express a mutated gene product with the desired activity. One
CC or more clonal populations of the identified cells is established, and
CC cells with an improved activity of interest are selected. These steps may
CC be iteratively repeated until a gene product with a desired of activity
CC is obtained. The cell lines prepared according to the method of the
CC invention are used for directed constitutive hypermutation of a nucleic
CC acid region in the preparation of a gene product, preferably an enzyme or
CC an immunoglobulin (Ig) with a desired activity. In the exemplifications
CC of the invention, IgM-secreting Ramos cells were selected for use as they
CC undergo hypermutation during clonal expansion. The present sequence
CC represents a mutant IgM light chain variable region (VL) from a Ramos
CC cell which binds streptavidin. The cell is the product of 4 rounds of
CC clonal expansion, hypermutation and selection
XX
SQ Sequence 100 AA;

Query Match 15.6%; Score 17; DB 3; Length 100;
Best Local Similarity 100.0%; Pred. No. 1e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GSPGQSITISCTGTSSD 28
||||||||||||||||
Db 6 GSPGQSITISCTGTSSD 22

RESULT 25
AAG93626
ID AAG93626 standard; protein; 104 AA.
XX
AC AAG93626;
XX
DT 14-SEP-2001 (first entry)
XX
DE Human anti-Rh(D) chain S01 protein sequence.
XX
KW Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;
KW red blood cell; Rh phenotype; diagnosis; therapeutic.
XX
OS Homo sapiens.
XX
PN US6255455-B1.
XX
PD 03-JUL-2001.
XX
PF 29-JAN-1999; 99US-00240274.
XX
PR 11-OCT-1996; 96US-0028550P.
PR 27-JUN-1997; 97US-00884045.
PR 10-APR-1998; 98US-0081380P.
XX
PA (UYPE-) UNIV PENNSYLVANIA.
XX
PI Siegel DL;
XX
DR WPI; 2001-388931/41.
DR N-PSDB; AAH68683.
XX
PT New isolated protein, preferably a human anti-Rh(D) antibody for use in
PT diagnostics requiring a human instead of an animal antibody and in
PT therapeutic medicine.

XX
PS Claim 1; Col 46; 162pp; English.
XX
CC The present invention describes an isolated Rh(D) binding protein,
CC preferably a human antibody. (I) having an amino acid sequence comprising
CC one of the sequences (S) given in AAG93558 to AAG93669. (I) has
CC immunostimulant activity, and can be used as an immune system stimulant.
CC (I) can be used in diagnostic and therapeutic medicine. The antibodies
CC are used in diagnostics that require human antibodies instead of animal
CC antibodies, such as determine the Rh phenotype of human red blood cells.
CC AAH68615 to AAH68726 represent the nucleotide sequence which encode
CC AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy
CC chain CDR3 amino acid sequences which are given in the exemplification of
CC the present invention
XX
SQ Sequence 104 AA;

Query Match 15.6%; Score 17; DB 4; Length 104;
Best Local Similarity 100.0%; Pred. No. 1e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 72 TASLTISGLQAEDEADY 88
||||||||||||||||
Db 67 TASLTISGLQAEDEADY 83

Search completed: March 15, 2004, 07:42:05
Job time : 57 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: March 15, 2004, 07:40:59 ; Search time 23 Seconds
(without alignments)
244.662 Million cell updates/sec

Title: US-09-620-955B-4
Perfect score: 109
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Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 389414 seqs, 51625971 residues

Word size : 0

Total number of hits satisfying chosen parameters: 270590

Minimum DB seq length: 0
Maximum DB seq length: 109

Post-processing: Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	26	23.9	104	1	US-08-488-113B-153	Sequence 153, App
2	26	23.9	104	1	US-08-477-484B-153	Sequence 153, App
3	26	23.9	104	1	US-08-107-669D-17	Sequence 17, Appl
4	26	23.9	104	1	US-08-472-788A-17	Sequence 17, Appl
5	26	23.9	104	2	US-08-477-531B-17	Sequence 17, Appl
6	26	23.9	104	2	US-08-646-360-153	Sequence 153, App
7	26	23.9	104	2	US-08-082-842A-17	Sequence 17, Appl
8	26	23.9	104	3	US-08-839-765-153	Sequence 153, App
9	26	23.9	104	3	US-09-136-389-153	Sequence 153, App
10	26	23.9	104	4	US-09-610-838-153	Sequence 153, App
11	26	23.9	104	4	US-09-711-485-153	Sequence 153, App
12	19	17.4	64	2	US-08-765-179B-10	Sequence 19, Appl
13	19	17.4	109	2	US-09-157-370-5	Sequence 5, Appli
14	17	15.6	104	3	US-09-240-274-69	Sequence 69, Appl
15	17	15.6	108	3	US-09-240-274-68	Sequence 68, Appl
16	12	11.0	103	1	US-07-942-245-8	Sequence 8, Appli
17	12	11.0	103	1	US-08-107-669D-3	Sequence 3, Appli
18	12	11.0	103	1	US-08-472-788A-3	Sequence 3, Appli
19	12	11.0	103	2	US-08-477-531B-3	Sequence 3, Appli
20	12	11.0	103	2	US-08-082-842A-3	Sequence 3, Appli
21	12	11.0	103	3	US-08-992-176-3	Sequence 3, Appli
22	12	11.0	104	3	US-09-240-274-49	Sequence 49, Appl
23	11	10.1	64	2	US-08-765-179B-10	Sequence 10, Appl
24	11	10.1	76	3	US-08-851-362D-20	Sequence 20, Appl
25	11	10.1	95	2	US-08-290-592E-19	Sequence 19, Appl
26	11	10.1	95	2	US-08-290-592E-33	Sequence 33, Appl
27	11	10.1	95	5	PCT-US95-10053-16	Sequence 16, Appl
28	11	10.1	95	5	PCT-US95-10053-30	Sequence 30, Appl
29	11	10.1	95	5	PCT-US96-09448-19	Sequence 19, Appl
30	11	10.1	95	5	PCT-US96-09448-33	Sequence 33, Appl
31	11	10.1	96	1	US-08-488-113B-158	Sequence 158, App
32	11	10.1	96	1	US-08-477-484B-158	Sequence 158, App
33	11	10.1	96	1	US-08-107-669D-22	Sequence 22, Appl
34	11	10.1	96	1	US-08-472-788A-22	Sequence 22, Appl
35	11	10.1	96	2	US-08-477-531B-22	Sequence 22, Appl
36	11	10.1	96	2	US-08-646-360-158	Sequence 158, App
37	11	10.1	96	2	US-08-082-842A-22	Sequence 22, Appl
38	11	10.1	96	3	US-08-839-765-158	Sequence 158, App
39	11	10.1	96	3	US-09-136-389-158	Sequence 158, App
40	11	10.1	96	4	US-09-610-838-158	Sequence 158, App
41	11	10.1	96	4	US-09-711-485-158	Sequence 158, App
42	11	10.1	105	3	US-08-851-362D-28	Sequence 28, Appl
43	11	10.1	105	3	US-08-851-362D-38	Sequence 38, Appl
44	11	10.1	106	1	US-07-634-278-35	Sequence 35, Appl
45	11	10.1	106	1	US-07-634-278-59	Sequence 59, Appl
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47	11	10.1	106	1	US-08-477-728-59	Sequence 59, Appl
48	11	10.1	106	1	US-08-474-040-35	Sequence 35, Appl
49	11	10.1	106	1	US-08-474-040-59	Sequence 59, Appl
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52	11	10.1	106	3	US-08-484-537-35	Sequence 35, Appl
53	11	10.1	106	3	US-08-484-537-59	Sequence 59, Appl
54	11	10.1	106	3	US-08-619-491-9	Sequence 9, Appli
55	11	10.1	106	4	US-09-771-415-1	Sequence 1, Appli
56	11	10.1	106	4	US-09-771-415-17	Sequence 17, Appl
57	11	10.1	106	4	US-09-771-415-19	Sequence 19, Appl
58	11	10.1	106	4	US-09-771-415-21	Sequence 21, Appl
59	11	10.1	106	4	US-09-771-415-23	Sequence 23, Appl
60	11	10.1	106	4	US-09-771-415-25	Sequence 25, Appl
61	11	10.1	106	5	PCT-US95-07302-9	Sequence 9, Appli
62	11	10.1	107	1	US-08-276-852-107	Sequence 107, App
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65	11	10.1	107	1	US-08-899-575-108	Sequence 108, App
66	11	10.1	107	1	US-08-899-575-107	Sequence 107, App
67	11	10.1	107	1	US-08-899-575-108	Sequence 108, App
68	11	10.1	107	2	US-08-303-569B-25	Sequence 25, Appl
69	11	10.1	107	2	US-08-070-116A-8	Sequence 8, Appli
70	11	10.1	107	2	US-08-116-247-26	Sequence 26, Appl
71	11	10.1	107	4	US-08-557-050-8	Sequence 8, Appli
72	11	10.1	107	4	US-09-795-515-25	Sequence 25, Appl
73	11	10.1	107	5	PCT-US95-08743-107	Sequence 107, App
74	11	10.1	107	5	PCT-US95-08743-108	Sequence 108, App
75	11	10.1	109	3	US-09-157-370-3	Sequence 3, Appli
76	10	9.2	13	3	US-08-466-368-13	Sequence 13, Appl
77	10	9.2	13	4	US-08-470-998-10	Sequence 10, Appl
78	10	9.2	13	4	US-08-328-500-18	Sequence 18, Appl
79	10	9.2	15	1	US-07-942-245-8	Sequence 8, Appli
80	10	9.2	15	1	US-08-137-117D-121	Sequence 121, App
81	10	9.2	15	1	US-08-137-117D-140	Sequence 140, App
82	10	9.2	15	2	US-08-436-717-121	Sequence 121, App
83	10	9.2	15	2	US-08-436-717-140	Sequence 140, App
84	10	9.2	15	2	US-08-553-501A-66	Sequence 66, Appl
85	10	9.2	15	2	US-08-553-501A-70	Sequence 70, Appl
86	10	9.2	15	2	US-08-318-157B-27	Sequence 27, Appl
87	10	9.2	15	2	US-08-560-558B-2	Sequence 2, Appli
88	10	9.2	15	2	US-08-765-179B-88	Sequence 88, Appl
89	10	9.2	15	3	US-08-470-139-11	Sequence 11, Appl
90	10	9.2	15	3	US-08-649-100-28	Sequence 28, Appl
91	10	9.2	15	3	US-09-205-231-66	Sequence 66, Appl
92	10	9.2	15	3	US-09-205-231-70	Sequence 70, Appl
93	10	9.2	15	3	US-08-569-147-38	Sequence 38, Appl
94	10	9.2	15	3	US-09-416-557-88	Sequence 88, Appl
95	10	9.2	15	4	US-09-347-061-11	Sequence 11, Appl
96	10	9.2	15	4	US-09-425-638A-85	Sequence 85, Appl
97	10	9.2	15	4	US-09-425-638A-86	Sequence 86, Appl
98	10	9.2	15	4	US-09-543-004-85	Sequence 85, Appl
99	10	9.2	15	4	US-09-543-004-86	Sequence 86, Appl
100	10	9.2	15	4	US-09-217-268B-2	Sequence 2, Appli

ALIGNMENTS

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RESULT 1
US-08-488-113B-153
; Sequence 153, Application US/08488113B
; Patent No. 5744580
;  GENERAL INFORMATION:
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Stephen F.
;    APPLICANT:  Studnika, Gary M.
;    TITLE OF INVENTION:  Immunotoxins Comprising Ribosome-Inactivating
;    TITLE OF INVENTION:  Proteins
;    NUMBER OF SEQUENCES:  169
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McAndrews, Held & Malloy, Ltd.
;      STREET:  500 West Madison Street, 34th floor
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60661
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/488,113B
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/425,336
;      FILING DATE:  18-APR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/064,691
;      FILING DATE:  12-MAY-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/988,430
;      FILING DATE:  09-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/901,707
;      FILING DATE:  19-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/787,567
;      FILING DATE:  04-NOV-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McNicholas, Janet M.
;      REGISTRATION NUMBER:  32,918
;      REFERENCE/DOCKET NUMBER:  11022US07/200-70.P3.C2A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/707-8889
;      TELEFAX:  312/707-9155
;      TELEX:  650 388-1248
;  INFORMATION FOR SEQ ID NO:  153:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  104 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-488-113B-153

  Query Match           23.9%;  Score 26;  DB 1;  Length 104;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-17;
  Matches   26;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 SALTQPASVSGSPGQSITISCTGTSS 27
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Db          2 SALTQPASVSGSPGQSITISCTGTSS 27


RESULT 2
US-08-477-484B-153
; Sequence 153, Application US/08477484B
; Patent No. 5756699
;  GENERAL INFORMATION:
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Stephen F.
;    APPLICANT:  Studnika, Gary M.
;    TITLE OF INVENTION:  Immunotoxins Comprising Ribosome-Inactivating
;    TITLE OF INVENTION:  Proteins
;    NUMBER OF SEQUENCES:  169
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McAndrews, Held & Malloy, Ltd.
;      STREET:  500 West Madison Street, 34th floor
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60661
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/477,484B
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/425,336
;      FILING DATE:  18-APR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/064,691
;      FILING DATE:  12-MAY-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/988,430
;      FILING DATE:  09-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/901,707
;      FILING DATE:  19-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/787,567
;      FILING DATE:  04-NOV-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McNicholas, Janet M.
;      REGISTRATION NUMBER:  32,918
;      REFERENCE/DOCKET NUMBER:  11022US07/200-70.P3.C2A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/707-8889
;      TELEFAX:  312/707-5155
;      TELEX:  650 388-1248
;  INFORMATION FOR SEQ ID NO:  153:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  104 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-477-484B-153

  Query Match           23.9%;  Score 26;  DB 1;  Length 104;
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Db          2 SALTQPASVSGSPGQSITISCTGTSS 27


RESULT 3
US-08-107-669D-17
; Sequence 17, Application US/08107669D
; Patent No. 5766886
;  GENERAL INFORMATION:
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;    APPLICANT:  Studnicka, Gary M.
;    TITLE OF INVENTION:  Modified Antibody Variable Domains (as amended)
;    NUMBER OF SEQUENCES:  67
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein and Fox P.L.L.C.
;      STREET:  1100 New York Ave., N.W., Suite 600
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  United States of America
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/107,669D
;      FILING DATE:  13-AUG-1993
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US92/10906
;      FILING DATE:  14-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/808,464
;      FILING DATE:  13-DEC-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Michele A. Cimbala
;      REGISTRATION NUMBER:  33,851
;      REFERENCE/DOCKET NUMBER:  0610.1000001/MAC
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202/371-2600
;      TELEFAX:  202/371-2540
;  INFORMATION FOR SEQ ID NO:  17:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  104 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-107-669D-17

  Query Match           23.9%;  Score 26;  DB 1;  Length 104;
  Best Local Similarity  100.0%;  Pred. No. 2.4e-17;
  Matches   26;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db          2 SALTQPASVSGSPGQSITISCTGTSS 27


RESULT 4
US-08-472-788A-17
; Sequence 17, Application US/08472788A
; Patent No. 5770196
;  GENERAL INFORMATION:
;    APPLICANT:  Studnicka, Gary M.
;    TITLE OF INVENTION:  Modified Antibody Variable Domains
;    NUMBER OF SEQUENCES:  89
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein and Fox P.L.L.C.
;      STREET:  1100 New York Ave., N.W., Suite 600
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/472,788A
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/082,842
;      FILING DATE:  23-JUN-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US92/10906
;      FILING DATE:  14-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/808,464
;      FILING DATE:  13-DEC-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Cimbala, Michele A.
;      REGISTRATION NUMBER:  33,851
;      REFERENCE/DOCKET NUMBER:  0610.1000003
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202/371-2600
;      TELEFAX:  202/371-2540
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  17:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  104 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-472-788A-17

  Query Match           23.9%;  Score 26;  DB 1;  Length 104;
  Best Local Similarity  100.0%;  Pred. No. 2.4e-17;
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Qy          2 SALTQPASVSGSPGQSITISCTGTSS 27
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Db          2 SALTQPASVSGSPGQSITISCTGTSS 27


RESULT 5
US-08-477-531B-17
; Sequence 17, Application US/08477531B
; Patent No. 5821123
;  GENERAL INFORMATION:
;    APPLICANT:  Studnicka, Gary M.
;    TITLE OF INVENTION:  Modified Antibody Variable Domains (as amended)
;    NUMBER OF SEQUENCES:  67
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein and Fox P.L.L.C.
;      STREET:  1100 New York Ave., N.W., Suite 600
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  United States of America
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/477,531B
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  436
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/107,669
;      FILING DATE:  13-AUG-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US92/10906
;      FILING DATE:  14-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/808,464
;      FILING DATE:  13-DEC-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Michele A. Cimbala
;      REGISTRATION NUMBER:  33,851
;      REFERENCE/DOCKET NUMBER:  0610.1000004/MAC
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202/371-2600
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;     TELEFAX:  202/371-2540
;   INFORMATION FOR SEQ ID NO:  17:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  104 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-477-531B-17

  Query Match           23.9%;  Score 26;  DB 2;  Length 104;
  Best Local Similarity  100.0%;  Pred. No. 2.4e-17;
  Matches   26;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 SALTQPASVSGSPGQSITISCTGTSS 27
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Db          2 SALTQPASVSGSPGQSITISCTGTSS 27


RESULT 6
US-08-646-360-153
; Sequence 153, Application US/08646360
; Patent No. 5837491
;  GENERAL INFORMATION:
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Stephen F.
;    APPLICANT:  Studnika, Gary M.
;    TITLE OF INVENTION:  Immunotoxins Comprising Ribosome-Inactivating
;    TITLE OF INVENTION:  Proteins
;    NUMBER OF SEQUENCES:  173
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McAndrews, Held & Malloy, Ltd.
;      STREET:  500 West Madison Street, 34th floor
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60661
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/646,360
;      FILING DATE:  13-MAY-1996
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US94/05348
;      FILING DATE:  12-MAY-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/064,691
;      FILING DATE:  12-MAY-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/988,430
;      FILING DATE:  09-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/901,707
;      FILING DATE:  19-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/787,567
;      FILING DATE:  04-NOV-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McNicholas, Janet M.
;      REGISTRATION NUMBER:  32,918
;      REFERENCE/DOCKET NUMBER:  200-70.P4
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/707-8889
;      TELEFAX:  312/707-9155
;      TELEX:  650 388-1248
;  INFORMATION FOR SEQ ID NO:  153:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  104 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-646-360-153

  Query Match           23.9%;  Score 26;  DB 2;  Length 104;
  Best Local Similarity  100.0%;  Pred. No. 2.4e-17;
  Matches   26;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 SALTQPASVSGSPGQSITISCTGTSS 27
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Db          2 SALTQPASVSGSPGQSITISCTGTSS 27


RESULT 7
US-08-082-842A-17
; Sequence 17, Application US/08082842A
; Patent No. 5869619
;  GENERAL INFORMATION:
;    APPLICANT:  Studnicka, Gary M.
;    TITLE OF INVENTION:  Modified Antibody Variable Domains
;    NUMBER OF SEQUENCES:  89
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein and Fox P.L.L.C.
;      STREET:  1100 New York Ave., N.W., Suite 600
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/082,842A
;      FILING DATE:  23-JUN-1993
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US92/10906
;      FILING DATE:  14-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/808,464
;      FILING DATE:  13-DEC-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Cimbala, Michele A.
;      REGISTRATION NUMBER:  33,851
;      REFERENCE/DOCKET NUMBER:  0610.1000002
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202/371-2600
;      TELEFAX:  202/371-2540
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  17:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  104 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-082-842A-17

  Query Match           23.9%;  Score 26;  DB 2;  Length 104;
  Best Local Similarity  100.0%;  Pred. No. 2.4e-17;
  Matches   26;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 SALTQPASVSGSPGQSITISCTGTSS 27
              |||||||||||||||||||||||||||
Db          2 SALTQPASVSGSPGQSITISCTGTSS 27


RESULT 8
US-08-839-765-153
; Sequence 153, Application US/08839765
; Patent No. 6146631
;  GENERAL INFORMATION:
```

```
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Stephen F.
;    APPLICANT:  Studnika, Gary M.
;    TITLE OF INVENTION:  Immunotoxins Comprising Ribosome-Inactivating
;    TITLE OF INVENTION:  Proteins
;    NUMBER OF SEQUENCES:  169
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McAndrews, Held & Malloy, Ltd.
;      STREET:  500 West Madison Street, 34th floor
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60661
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/839,765
;      FILING DATE:  15-APR-1997
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/425,336
;      FILING DATE:  18-APR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/064,691
;      FILING DATE:  12-MAY-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/988,430
;      FILING DATE:  09-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/901,707
;      FILING DATE:  19-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/787,567
;      FILING DATE:  04-NOV-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McNicholas, Janet M.
;      REGISTRATION NUMBER:  32,918
;      REFERENCE/DOCKET NUMBER:  11022US09/200-70.P3.C3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/707-8889
;      TELEFAX:  312/707-9155
;      TELEX:  650 388-1248
;  INFORMATION FOR SEQ ID NO:  153:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  104 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-839-765-153

  Query Match           23.9%;  Score 26;  DB 3;  Length 104;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-17;
  Matches   26;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 SALTQPASVSGSPGQSITISCTGTSS 27
              ||||||||||||||||||||||||||
Db          2 SALTQPASVSGSPGQSITISCTGTSS 27


RESULT 9
US-09-136-389-153
; Sequence 153, Application US/09136389
; Patent No. 6146850
;  GENERAL INFORMATION:
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Stephen F.
;    APPLICANT:  Studnika, Gary M.
;    TITLE OF INVENTION:  Immunotoxins Comprising Ribosome-Inactivating
;    TITLE OF INVENTION:  Proteins
;    NUMBER OF SEQUENCES:  173
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McAndrews, Held & Malloy, Ltd.
;      STREET:  500 West Madison Street, 34th floor
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60661
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/136,389
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/646,360
;      FILING DATE:  13-MAY-1996
;      APPLICATION NUMBER:  PCT/US94/05348
;      FILING DATE:  12-MAY-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/064,691
;      FILING DATE:  12-MAY-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/988,430
;      FILING DATE:  09-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/901,707
;      FILING DATE:  19-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/787,567
;      FILING DATE:  04-NOV-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McNicholas, Janet M.
;      REGISTRATION NUMBER:  32,918
;      REFERENCE/DOCKET NUMBER:  200-70.P4
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/707-8889
;      TELEFAX:  312/707-9155
;      TELEX:  650 388-1248
;  INFORMATION FOR SEQ ID NO:  153:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  104 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-136-389-153

  Query Match           23.9%;  Score 26;  DB 3;  Length 104;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-17;
  Matches   26;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 SALTQPASVSGSPGQSITISCTGTSS 27
              ||||||||||||||||||||||||||
Db          2 SALTQPASVSGSPGQSITISCTGTSS 27


RESULT 10
US-09-610-838-153
; Sequence 153, Application US/09610838
; Patent No. 6376217
;  GENERAL INFORMATION:
;    APPLICANT:  Better, Marc D.
;    APPLICANT:  Carroll, Stephen F.
;    APPLICANT:  Studnika, Gary M.
;    TITLE OF INVENTION:  Immunotoxins Comprising Ribosome-Inactivating
;    TITLE OF INVENTION:  Proteins
;    NUMBER OF SEQUENCES:  173
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McAndrews, Held & Malloy, Ltd.
```

```
;       STREET:  500 West Madison Street, 34th floor
;       CITY:  Chicago
;       STATE:  Illinois
;       COUNTRY:  USA
;       ZIP:  60661
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/09/610,838
;       FILING DATE:  06-JUL-2000
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US/09/136,389
;       FILING DATE:  18-AUG-1998
;       APPLICATION NUMBER:  08/646,360
;       FILING DATE:  13-MAY-1996
;       APPLICATION NUMBER:  PCT/US94/05348
;       FILING DATE:  12-MAY-1994
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/064,691
;       FILING DATE:  12-MAY-1993
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/988,430
;       FILING DATE:  09-DEC-1992
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/901,707
;       FILING DATE:  19-JUN-1992
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/787,567
;       FILING DATE:  04-NOV-1991
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  McNicholas, Janet M.
;       REGISTRATION NUMBER:  32,918
;       REFERENCE/DOCKET NUMBER:  200-70.P4
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  312/707-8889
;       TELEFAX:  312/707-9155
;       TELEX:  650 388-1248
;   INFORMATION FOR SEQ ID NO:  153:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  104 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  double
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-09-610-838-153

  Query Match           23.9%;  Score 26;  DB 4;  Length 104;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+17;
  Matches   26;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 SALTQPASVSGSPGQSITISCTGTSS 27
              |||||||||||||||||||||||||||
Db          2 SALTQPASVSGSPGQSITISCTGTSS 27


RESULT 11
US-09-711-485-153
; Sequence 153, Application US/09711485
; Patent No. 6649742
;   GENERAL INFORMATION:
;     APPLICANT:  Better, Marc D.
;     APPLICANT:  Carroll, Stephen F.
;     APPLICANT:  Studnika, Gary M.
;     TITLE OF INVENTION:  Immunotoxins Comprising Ribosome-Inactivating
;     TITLE OF INVENTION:  Proteins
;     NUMBER OF SEQUENCES:  169
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  McAndrews, Held & Malloy, Ltd.
;       STREET:  500 West Madison Street, 34th floor
;       CITY:  Chicago
;       STATE:  Illinois
;       COUNTRY:  USA
;       ZIP:  60661
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/09/711,485
;       FILING DATE:
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/839,765
;       FILING DATE:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/064,691
;       FILING DATE:  12-MAY-1993
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/988,430
;       FILING DATE:  09-DEC-1992
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/901,707
;       FILING DATE:  19-JUN-1992
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/787,567
;       FILING DATE:  04-NOV-1991
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  McNicholas, Janet M.
;       REGISTRATION NUMBER:  32,918
;       REFERENCE/DOCKET NUMBER:  11022US09/200-70.P3.C3
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  312/707-8889
;       TELEFAX:  312/707-9155
;       TELEX:  650 388-1248
;   INFORMATION FOR SEQ ID NO:  153:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  104 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  double
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-09-711-485-153

  Query Match           23.9%;  Score 26;  DB 4;  Length 104;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+17;
  Matches   26;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 SALTQPASVSGSPGQSITISCTGTSS 27
              |||||||||||||||||||||||||||
Db          2 SALTQPASVSGSPGQSITISCTGTSS 27


RESULT 12
US-08-765-179B-19
; Sequence 19, Application US/08765179B
; Patent No. 5854027
;   GENERAL INFORMATION:
;     APPLICANT:  STEIPE, Boris
;     APPLICANT:  STEINBACHER, Stefan
;     TITLE OF INVENTION:  PROCESS FOR MODIFYING THE STABILITY
;     TITLE OF INVENTION:  OF ANTIBODIES
;     NUMBER OF SEQUENCES:  28
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Nikaido, Marmelstein, Murray & Oram LLP
;       STREET:  655 Fifteenth Street N.W. Suite 330
;       CITY:  Washington
;       STATE:  D.C.
;       COUNTRY:  U.S.A.
;       ZIP:  20005-5701
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
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;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/765,179B
;       FILING DATE:  14-JAN-1997
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/EP95/02626
;       FILING DATE:  06-JUL-1995
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  DE P 44 25 115.7
;       FILING DATE:  15-JUL-1994
;   INFORMATION FOR SEQ ID NO:  19:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  64 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-765-179B-19

  Query Match             17.4%;  Score 19;  DB 2;  Length 64;
  Best Local Similarity   100.0%;  Pred. No. 6.8e-11;
  Matches   19;  Conservative    0;  Mismatches   0;  Indels    0;  Gaps    0;

Qy          72 TASLTISGLQAEDEADYYC 90
               |||||||||||||||||||
Db          39 TASLTISGLQAEDEADYYC 57


RESULT 13
US-09-157-370-5
; Sequence 5, Application US/09157370A
; Patent No. 6262238
; GENERAL INFORMATION:
;  APPLICANT:  STRIPE, Boris
;  APPLICANT:  STEINBACHER, Stefan
;  TITLE OF INVENTION:  PROCESS FOR MODIFYING THE STABILITY OF ANTIBODIES
;  FILE REFERENCE:  P8341-8072
;  CURRENT APPLICATION NUMBER:  US/09/157,370A
;  CURRENT FILING DATE:  1998-09-21
;  EARLIER APPLICATION NUMBER:  08/765,179
;  EARLIER FILING DATE:  1997-01-14
;  EARLIER APPLICATION NUMBER:  PCT/EP95/02626
;  EARLIER FILING DATE:  1995-07-06
;  EARLIER APPLICATION NUMBER:  DE/P44 25 115.7
;  EARLIER FILING DATE:  1994-07-15
;  NUMBER OF SEQ ID NOS:  10
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 5
;   LENGTH:  109
;   TYPE:  PRT
;   ORGANISM:  Homo sapiens
US-09-157-370-5

  Query Match             17.4%;  Score 19;  DB 3;  Length 109;
  Best Local Similarity   100.0%;  Pred. No. 1e-10;
  Matches   19;  Conservative    0;  Mismatches   0;  Indels    0;  Gaps    0;

Qy          72 TASLTISGLQAEDEADYYC 90
               |||||||||||||||||||
Db          69 TASLTISGLQAEDEADYYC 87


RESULT 14
US-09-240-274-69
; Sequence 69, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
;  APPLICANT:  Siegel, Donald L.
;  TITLE OF INVENTION:  Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;  TITLE OF INVENTION:  SORTING METHOD FOR PRODUCTION THEREOF
;  FILE REFERENCE:  09596-42U2
;  CURRENT APPLICATION NUMBER:  US/09/240,274
;  CURRENT FILING DATE:  1999-01-29
;  EARLIER APPLICATION NUMBER:  60/081,380
;  EARLIER FILING DATE:  1998-04-10
;  EARLIER APPLICATION NUMBER:  60/028,550
;  EARLIER FILING DATE:  1996-10-11
;  NUMBER OF SEQ ID NOS:  224
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 69
;   LENGTH:  104
;   TYPE:  PRT
;   ORGANISM:  Homo sapiens
;   FEATURE:
;   OTHER INFORMATION:  anti-Rh(D) chain S01
US-09-240-274-69

  Query Match             15.6%;  Score 17;  DB 3;  Length 104;
  Best Local Similarity   100.0%;  Pred. No. 7.9e-09;
  Matches   17;  Conservative    0;  Mismatches   0;  Indels    0;  Gaps    0;

Qy          72 TASLTISGLQAEDEADY 88
               |||||||||||||||||
Db          67 TASLTISGLQAEDEADY 83


RESULT 15
US-09-240-274-68
; Sequence 68, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
;  APPLICANT:  Siegel, Donald L.
;  TITLE OF INVENTION:  Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;  TITLE OF INVENTION:  SORTING METHOD FOR PRODUCTION THEREOF
;  FILE REFERENCE:  09596-42U2
;  CURRENT APPLICATION NUMBER:  US/09/240,274
;  CURRENT FILING DATE:  1999-01-29
;  EARLIER APPLICATION NUMBER:  60/081,380
;  EARLIER FILING DATE:  1998-04-10
;  EARLIER APPLICATION NUMBER:  60/028,550
;  EARLIER FILING DATE:  1996-10-11
;  NUMBER OF SEQ ID NOS:  224
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 68
;   LENGTH:  108
;   TYPE:  PRT
;   ORGANISM:  Homo sapiens
;   FEATURE:
;   OTHER INFORMATION:  anti-Rh(D) chain R01
US-09-240-274-68

  Query Match             15.6%;  Score 17;  DB 3;  Length 108;
  Best Local Similarity   100.0%;  Pred. No. 8.2e-09;
  Matches   17;  Conservative    0;  Mismatches   0;  Indels    0;  Gaps    0;

Qy          78 SGLQAEDEADYYCSSFA 94
               |||||||||||||||||
Db          77 SGLQAEDEADYYCSSFA 93


RESULT 16
US-07-942-245-8
; Sequence 8, Application US/07942245
; Patent No. 5619641
;  GENERAL INFORMATION:
;    APPLICANT:  PEDERSEN, Jan T.
;    APPLICANT:  SEABLE,  Stephen M.J.
;    APPLICANT:  REES,    Anthony R.
;    APPLICANT:  ROGUSKA,  Michael A.
;    APPLICANT:  GUILD,    Braydon C.
;    TITLE OF INVENTION:  SURFACE RESIDUE VENEERING OF RODENT
;    TITLE OF INVENTION:  ANTIBODIES
;    NUMBER OF SEQUENCES:  522
```

```
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Sughrue, Mion, Zinn, Macpeak & Seas
;       STREET:  2100 Pensylvania Avenue, N.W.
;       CITY:  Washington
;       STATE:  D.C.
;       COUNTRY:  United States
;       ZIP:  20037-3202
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  HP 9000/700 Workstation
;       OPERATING SYSTEM:  UNIX
;       SOFTWARE:  In house
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/07/942,245
;       FILING DATE:  09-SEP-1992
;       CLASSIFICATION:  530
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (202) 293-7060
;       TELEFAX:  (202) 293-7860
;       TELEX:  6491103
;   INFORMATION FOR SEQ ID NO:  8:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  103 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
US-07-942-245-8

  Query Match           11.0%;  Score 12;  DB 1;  Length 103;
  Best Local Similarity  100.0%;  Pred. No. 0.00043;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          79 GLQAEDEADYYC 90
               ||||||||||||
Db          71 GLQAEDEADYYC 82


RESULT 17
US-08-107-669D-3
; Sequence 3, Application US/08107669D
; Patent No. 5766886
;  GENERAL INFORMATION:
;    APPLICANT:  Studnicka, Gary M.
;    TITLE OF INVENTION:  Modified Antibody Variable Domains (as amended)
;    NUMBER OF SEQUENCES:  67
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein and Fox P.L.L.C.
;      STREET:  1100 New York Ave., N.W., Suite 600
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  United States of America
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/107,669D
;      FILING DATE:  13-AUG-1993
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US92/10906
;      FILING DATE:  14-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/808,464
;      FILING DATE:  13-DEC-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Michele A. Cimbala
;      REGISTRATION NUMBER:  33,851
;      REFERENCE/DOCKET NUMBER:  0610.1000001/MAC
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202/371-2600
;      TELEFAX:  202/371-2540
;    INFORMATION FOR SEQ ID NO:  3:
;      SEQUENCE CHARACTERISTICS:
;        LENGTH:  103 amino acids
;        TYPE:  amino acid
;        TOPOLOGY:  linear
;      MOLECULE TYPE:  protein
US-08-107-669D-3

  Query Match           11.0%;  Score 12;  DB 1;  Length 103;
  Best Local Similarity  100.0%;  Pred. No. 0.00043;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          79 GLQAEDEADYYC 90
               ||||||||||||
Db          72 GLQAEDEADYYC 83


RESULT 18
US-08-472-788A-3
; Sequence 3, Application US/08472788A
; Patent No. 5770196
;  GENERAL INFORMATION:
;    APPLICANT:  Studnicka, Gary M.
;    TITLE OF INVENTION:  Modified Antibody Variable Domains
;    NUMBER OF SEQUENCES:  89
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein and Fox P.L.L.C.
;      STREET:  1100 New York Ave., N.W., Suite 600
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/472,788A
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/082,842
;      FILING DATE:  23-JUN-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US92/10906
;      FILING DATE:  14-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/808,464
;      FILING DATE:  13-DEC-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Cimbala, Michele A.
;      REGISTRATION NUMBER:  33,851
;      REFERENCE/DOCKET NUMBER:  0610.1000003
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202/371-2600
;      TELEFAX:  202/371-2540
;      TELEX:
;    INFORMATION FOR SEQ ID NO:  3:
;      SEQUENCE CHARACTERISTICS:
;        LENGTH:  103 amino acids
;        TYPE:  amino acid
;        TOPOLOGY:  linear
;      MOLECULE TYPE:  protein
US-08-472-788A-3

  Query Match           11.0%;  Score 12;  DB 1;  Length 103;
  Best Local Similarity  100.0%;  Pred. No. 0.00043;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          79 GLQAEDEADYYC 90
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Db          72 GLQAEDEADYYC 83


RESULT 19
US-08-477-531B-3
; Sequence 3, Application US/08477531B
; Patent No. 5821123
;  GENERAL INFORMATION:
;    APPLICANT:  Studnicka, Gary M.
;    TITLE OF INVENTION:  Modified Antibody Variable Domains (as amended)
;    NUMBER OF SEQUENCES:  67
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein and Fox P.L.L.C.
;      STREET:  1100 New York Ave., N.W., Suite 600
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  United States of America
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/477,531B
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  436
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/107,669
;      FILING DATE:  13-AUG-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US92/10906
;      FILING DATE:  14-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/808,464
;      FILING DATE:  13-DEC-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Michele A. Cimbala
;      REGISTRATION NUMBER:  33,851
;      REFERENCE/DOCKET NUMBER:  0610.1000004/MAC
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202/371-2600
;      TELEFAX:  202/371-2540
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  103 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-477-531B-3

  Query Match             11.0%;  Score 12;  DB 2;  Length 103;
  Best Local Similarity   100.0%;  Pred. No. 0.00043;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          79 GLQAEDEADYYC 90
               ||||||||||||
Db          72 GLQAEDEADYYC 83


RESULT 20
US-08-082-842A-3
; Sequence 3, Application US/08082842A
; Patent No. 5869619
;  GENERAL INFORMATION:
;    APPLICANT:  Studnicka, Gary M.
;    TITLE OF INVENTION:  Modified Antibody Variable Domains
;    NUMBER OF SEQUENCES:  89
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein and Fox P.L.L.C.
;      STREET:  1100 New York Ave., N.W., Suite 600
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/082,842A
;      FILING DATE:  23-JUN-1993
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US92/10906
;      FILING DATE:  14-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/808,464
;      FILING DATE:  13-DEC-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Cimbala, Michele A.
;      REGISTRATION NUMBER:  33,851
;      REFERENCE/DOCKET NUMBER:  0610.1000002
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202/371-2600
;      TELEFAX:  202/371-2540
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  103 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-082-842A-3

  Query Match             11.0%;  Score 12;  DB 2;  Length 103;
  Best Local Similarity   100.0%;  Pred. No. 0.00043;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          79 GLQAEDEADYYC 90
               ||||||||||||
Db          72 GLQAEDEADYYC 83


RESULT 21
US-08-992-176-3
; Sequence 3, Application US/08992176
; Patent No. 6123331
; GENERAL INFORMATION:
;  APPLICANT: TON, Hiroyuki
;  TITLE OF INVENTION: STRUCTURAL ALIGNMENT METHOD MAKING USE OF A DOUBLE
;  TITLE OF INVENTION: DYNAMIC PROGRAMMING ALGORITHM
;  FILE REFERENCE: 9200-0001-2
;  CURRENT APPLICATION NUMBER: US/08/992,176
;  CURRENT FILING DATE: 1997-12-17
;  EARLIER APPLICATION NUMBER: JP 8-340727
;  EARLIER FILING DATE: 1996-12-20
;  NUMBER OF SEQ ID NOS: 10
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 103
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:beta-protein
;   OTHER INFORMATION: (7Eabl)
US-08-992-176-3

  Query Match             11.0%;  Score 12;  DB 3;  Length 103;
  Best Local Similarity   100.0%;  Pred. No. 0.00043;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          79 GLQAEDEADYYC 90
               ||||||||||||
Db          72 GLQAEDEADYYC 83
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```
RESULT 22
US-09-240-274-49
; Sequence 49, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
;  APPLICANT: Siegel, Donald L.
;  TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;  TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
;  FILE REFERENCE: 09596-42U2
;  CURRENT APPLICATION NUMBER: US/09/240,274
;  CURRENT FILING DATE: 1999-01-29
;  EARLIER APPLICATION NUMBER: 60/081,380
;  EARLIER FILING DATE: 1998-04-10
;  EARLIER APPLICATION NUMBER: 60/028,550
;  EARLIER FILING DATE: 1996-10-11
;  NUMBER OF SEQ ID NOS: 224
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 49
;   LENGTH: 104
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: anti-Rh(D) chain J04
US-09-240-274-49

  Query Match             11.0%;  Score 12;  DB 3;  Length 104;
  Best Local Similarity   100.0%;  Pred. No. 0.00043;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         81 QAEDSADTYCSS 92
               ||||||||||||
Db         76 QAEDSADTYCSS 87


RESULT 23
US-08-765-179B-10
; Sequence 10, Application US/08765179B
; Patent No. 5854027
;  GENERAL INFORMATION:
;    APPLICANT:  STEIPE, Boris
;    APPLICANT:  STEINBACHER, Stefan
;    TITLE OF INVENTION:  PROCESS FOR MODIFYING THE STABILITY
;    TITLE OF INVENTION:  OF ANTIBODIES
;    NUMBER OF SEQUENCES:  28
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Nikaido, Marmelstein, Murray & Oram LLP
;      STREET:  655 Fifteenth Street N.W. Suite 330
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20005-5701
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/765,179B
;      FILING DATE:  14-JAN-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/EP95/02626
;      FILING DATE:  06-JUL-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  DE P 44 25 115.7
;      FILING DATE:  15-JUL-1994
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  64 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-765-179B-10

  Query Match             10.1%;  Score 11;  DB 2;  Length 64;
  Best Local Similarity   100.0%;  Pred. No. 0.0026;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         42 PGKAPKLLIYD 52
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Db          9 PGKAPKLLIYD 19


RESULT 24
US-08-851-362D-20
; Sequence 20, Application US/08851362D
; Patent No. 6235883
; GENERAL INFORMATION:
;  APPLICANT:  Jakobovits, Aya
;  APPLICANT:  Yang, Xiao-Dong
;  APPLICANT:  Gallo, Michael
;  APPLICANT:  Jia, Xiao-Chi
;  TITLE OF INVENTION:  Human Monoclonal Antibodies to Epidermal
;  TITLE OF INVENTION:  Growth Factor Receptor
;  FILE REFERENCE:  Cell 4.20
;  CURRENT APPLICATION NUMBER: US/08/851,362D
;  CURRENT FILING DATE:  1997-05-05
;  NUMBER OF SEQ ID NOS:  49
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 20
;   LENGTH:  76
;   TYPE:  PRT
;   ORGANISM:  human
US-08-851-362D-20

  Query Match             10.1%;  Score 11;  DB 3;  Length 76;
  Best Local Similarity   100.0%;  Pred. No. 0.0029;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         42 PGKAPKLLIYD 52
               ||||||||||||
Db         21 PGKAPKLLIYD 31


RESULT 25
US-08-290-592E-19
; Sequence 19, Application US/08290592E
; Patent No. 5824307
;  GENERAL INFORMATION:
;    APPLICANT:  JOHNSON, L.
;    TITLE OF INVENTION:  Human Murine Chimeric Antibodies Against
;    TITLE OF INVENTION:  Respiratory Syncytical Virus
;    NUMBER OF SEQUENCES:  49
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CABELLA, BYRNE, BAIN, GILFILLAN, CECCHI, STEWART &
;      ADDRESSEE:  OLSTEIN
;      STREET:  6 BECKER FARM ROAD
;      CITY:  ROSELAND
;      STATE:  NEW JERSEY
;      COUNTRY:  USA
;      ZIP:  07068
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 INCH DISKETTE
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/290,592E
;      FILING DATE:  August 15, 1994
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/813,372
;      FILING DATE:  December 23, 1991
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;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Olstein, Elliot M.
;      REGISTRATION NUMBER:  24,025
;      REFERENCE/DOCKET NUMBER:  469201-257
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-994-1700
;      TELEFAX:  201-994-1744
; INFORMATION FOR SEQ ID NO:  19:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  95 AMINO ACIDS
;      TYPE:  AMINO ACID
;      TOPOLOGY:  LINEAR
;    MOLECULE TYPE:  PROTEIN
US-08-290-592E-19

  Query Match          10.1%;  Score 11;  DB 2;  Length 95;
  Best Local Similarity   100.0%;  Pred. No. 0.0035;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         42 PGKAPKLLIYD 52
              ||||||||||
Db         40 PGKAPKLLIYD 50


Search completed: March 15, 2004, 07:44:32
Job time : 24 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: March 15, 2004, 07:40:14 ; Search time 20 Seconds
(without alignments)
524.244 Million cell updates/sec

Title: US-09-620-955B-4
Perfect score: 109
Sequence: 1 QSALTQPASVSGSPQQSITI.....CSSPANSGPLPGGGTKVTVL 109

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283366 seqs, 96191526 residues

Word size : 0

Total number of hits satisfying chosen parameters: 44099

Minimum DB seq length: 0
Maximum DB seq length: 109

Post-processing: Listing first 100 summaries

Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	28	25.7	99	2	S36055	Ig lambda chain -
2	28	25.7	99	2	S36056	Ig lambda chain -
3	20	18.3	99	2	S36058	Ig lambda chain -
4	19	17.4	99	2	S36057	Ig lambda chain -
5	19	17.4	109	1	L2HUBR	Ig lambda chain V-
6	12	11.0	99	2	S36051	Ig lambda chain -
7	12	11.0	99	2	S36052	Ig lambda chain -
8	12	11.0	99	2	S36053	Ig lambda chain -
9	12	11.0	103	1	L1HUNM	Ig lambda chain V-
10	11	10.1	62	2	S42265	Ig kappa chain V r
11	11	10.1	87	2	I52592	Ig kappa chain V r
12	11	10.1	88	2	S34088	Ig kappa chain V r
13	11	10.1	88	2	S34087	Ig kappa chain V r
14	11	10.1	95	2	PH0862	Ig kappa chain V-I
15	11	10.1	95	2	PH0864	Ig kappa chain V r
16	11	10.1	107	2	B46516	Ig lambda chain V
17	11	10.1	108	1	K1HUAU	Ig kappa chain V-I
18	11	10.1	108	1	K1HURY	Ig kappa chain V-I
19	10	9.2	53	2	PH0881	Ig kappa chain V r
20	10	9.2	60	2	A24626	Ig lambda chain V-
21	10	9.2	65	2	PH0880	Ig kappa chain V r
22	10	9.2	82	2	S34090	Ig kappa chain V r
23	10	9.2	86	2	S34086	Ig kappa chain V r
24	10	9.2	86	2	S16840	Ig kappa chain V r
25	10	9.2	87	2	S21523	Ig kappa chain V r
26	10	9.2	87	2	S34084	Ig kappa chain V r
27	10	9.2	87	2	S34083	Ig kappa chain V r
28	10	9.2	88	2	S21528	Ig kappa chain V r
29	10	9.2	88	2	S21524	Ig kappa chain V r
30	10	9.2	88	2	S21520	Ig kappa chain V r
31	10	9.2	88	2	S21522	Ig kappa chain V r
32	10	9.2	88	2	S34104	Ig kappa chain V r
33	10	9.2	92	2	A27633	Ig lambda-2 chain
34	10	9.2	96	2	S36060	Ig lambda chain -
35	10	9.2	98	2	S36046	Ig lambda chain -
36	10	9.2	98	2	S41813	Ig kappa chain V r
37	10	9.2	99	2	S36059	Ig lambda chain -
38	10	9.2	103	2	A38923	AL type amyloid fi
39	10	9.2	103	2	S18731	Ig kappa chain V-J
40	10	9.2	105	2	S49533	anti-Sm antibody V
41	10	9.2	106	2	S38495	Ig lambda chain -
42	10	9.2	106	2	S40091	Ig light chain - m
43	10	9.2	106	2	PC2397	anti-tetanus toxin
44	10	9.2	107	1	L4HUHL	Ig lambda chain V-
45	10	9.2	107	2	S36264	Ig lambda chain V
46	10	9.2	107	2	S36262	Ig lambda chain V
47	10	9.2	107	2	S36269	Ig lambda chain V
48	10	9.2	108	1	K1HURE	Ig kappa chain V-I
49	10	9.2	108	1	K1HUKA	Ig kappa chain V-I
50	10	9.2	108	1	KVMS61	Ig kappa chain V r
51	10	9.2	108	1	KVMS09	Ig kappa chain V r
52	10	9.2	108	1	KVMS06	Ig kappa chain V r
53	10	9.2	108	1	KVMS82	Ig kappa chain V r
54	10	9.2	108	1	L3HUSH	Ig lambda chain V-
55	10	9.2	108	2	S38498	Ig lambda chain -
56	10	9.2	108	2	S47184	Ig lambda chain -
57	10	9.2	108	2	S19674	Ig kappa chain V r
58	10	9.2	108	2	S31977	Ig lambda chain - h
59	10	9.2	108	2	B49047	Ig kappa chain V r
60	10	9.2	108	2	S47182	Ig kappa chain - h
61	10	9.2	108	2	S36277	Ig lambda chain V
62	10	9.2	108	2	S36279	Ig lambda chain V
63	10	9.2	109	2	S38496	Ig lambda chain -
64	10	9.2	109	2	S19663	Ig lambda chain V
65	10	9.2	109	2	S68171	Ig lambda chain V
66	10	9.2	109	2	S31998	Ig kappa chain - h
67	9	8.3	108	1	K1HUMS	Ig kappa chain V-I
68	9	8.3	108	2	S44122	Ig kappa chain V r
69	9	8.3	109	1	K1HUMV	Ig kappa chain V-I
70	9	8.3	109	2	S31981	Ig kappa chain - h
71	9	8.3	109	2	S31978	Ig kappa chain - h
72	9	8.3	109	2	S38494	Ig lambda chain -
73	9	8.3	109	2	JN0296	Ig kappa chain V-J
74	8	7.3	57	2	PH0879	Ig kappa chain V r
75	8	7.3	90	2	S24218	Ig kappa chain - m
76	8	7.3	94	2	C32529	Ig lambda chain V
77	8	7.3	95	2	S49571	Ig lambda chain pr
78	8	7.3	97	2	I51216	Ig light chain var
79	8	7.3	98	2	S36068	Ig lambda chain -
80	8	7.3	98	2	S36047	Ig lambda chain -
81	8	7.3	98	2	S36048	Ig lambda chain -
82	8	7.3	98	2	S36050	Ig lambda chain -
83	8	7.3	99	2	S36054	Ig lambda chain -
84	8	7.3	108	1	K1HUEU	Ig kappa chain V-I
85	8	7.3	108	1	K1HUEU	Ig kappa chain V-I
86	8	7.3	109	1	L1HUEP	Ig lambda chain V-
87	8	7.3	109	1	L1HUWA	Ig lambda chain V-
88	7	6.4	13	2	S03063	Ig lambda chain J
89	7	6.4	39	2	G32529	Ig lambda chain V
90	7	6.4	47	2	S32529	Ig lambda chain V
91	7	6.4	75	2	S40337	Ig kappa chain V-J
92	7	6.4	77	2	D30502	Ig kappa chain V r
93	7	6.4	91	2	PH1071	Ig light chain V r
94	7	6.4	91	2	S37525	Ig kappa chain V r
95	7	6.4	92	2	S37523	Ig kappa chain V r
96	7	6.4	92	2	S37535	Ig kappa chain V r
97	7	6.4	92	2	S37510	Ig kappa chain V r
98	7	6.4	92	2	S37532	Ig kappa chain V r
99	7	6.4	94	2	A01955	Ig kappa-B5 chain
100	7	6.4	95	2	S36065	Ig lambda chain -

ALIGNMENTS

RESULT 1
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Ig lambda chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 21-Jan-2000
C;Accession: S36055
R;Williams, S.C.
submitted to the EMBL Data Library, April 1993
A;Reference number: S36046
A;Accession: S36055
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-99 <WIL>
A;Cross-references: EMBL:Z22196; NID:g312856; PIDN:CAA80206.1; PID:g312857
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-92/Domain: immunoglobulin homology <IMM>

Query Match 25.7%; Score 28; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 5.4e-21;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QSALTQPASVSGSPGQSITISCTGTSSD 28
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Db 1 QSALTQPASVSGSPGQSITISCTGTSSD 28

RESULT 2
S36056
Ig lambda chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 21-Jan-2000
C;Accession: S36056
R;Williams, S.C.
submitted to the EMBL Data Library, April 1993
A;Reference number: S36046
A;Accession: S36056
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-99 <WIL>
A;Cross-references: EMBL:Z22197; NID:g312317; PIDN:CAA80207.1; PID:g312318
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-92/Domain: immunoglobulin homology <IMM>

Query Match 25.7%; Score 28; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 5.4e-21;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QSALTQPASVSGSPGQSITISCTGTSSD 28
||||||||||||||||||||||||||||
Db 1 QSALTQPASVSGSPGQSITISCTGTSSD 28

RESULT 3
S36058
Ig lambda chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 23-Jul-1999
C;Accession: S36058
R;Williams, S.C.
submitted to the EMBL Data Library, April 1993
A;Reference number: S36046
A;Accession: S36058
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-99 <WIL>
A;Cross-references: EMBL:Z22199; NID:g312858; PIDN:CAA80209.1; PID:g312859
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 18.3%; Score 20; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 7.4e-13;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 72 TASLTISGLQAEDEADYYCS 91
||||||||||||||||||||
Db 72 TASLTISGLQAEDEADYYCS 91

RESULT 4
S36057
Ig lambda chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 21-Jan-2000
C;Accession: S36057
R;Williams, S.C.
submitted to the EMBL Data Library, April 1993
A;Reference number: S36046
A;Accession: S36057
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-99 <WIL>
A;Cross-references: EMBL:Z22198; NID:g312319; PIDN:CAA80208.1; PID:g312320
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-92/Domain: immunoglobulin homology <IMM>

Query Match 17.4%; Score 19; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 7.6e-12;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 72 TASLTISGLQAEDEADYYC 90
|||||||||||||||||||
Db 72 TASLTISGLQAEDEADYYC 90

RESULT 5
L2HUBP
Ig lambda chain V-II region (Bur) - human
C;Species: Homo sapiens (man)
C;Date: 31-Mar-1980 #sequence_revision 31-Mar-1980 #text_change 02-Sep-1997
C;Accession: A01974
R;Infante, A.J.; Putnam, F.W.
J. Biol. Chem. 254, 9006-9016, 1979
A;Title: Primary structure of a human IgA1 immunoglobulin. V. Amino acid sequence of
A;Reference number: A01974; MUID:80006606; PMID:113407
A;Accession: A01974
A;Molecule type: protein
A;Residues: 1-109 <INF>
A;Note: Cys-91 appears to be a free but unreactive sulfhydryl group
A;Note: the C region of this chain has the Kern+ and Oxg- markers
C;Comment: This chain was isolated from a myeloma protein.
C;Genetics:
A;Gene: GDB:IGLV@
A;Cross-references: GDB:119342; OMIM:147240
A;Map position: 22q11.2-22q11.2
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate int
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin; pyroglutamic acid
F;15-92/Domain: immunoglobulin homology <IMM>
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;22-90/Disulfide bonds: #status predicted

Query Match 17.4%; Score 19; DB 1; Length 109;
Best Local Similarity 100.0%; Pred. No. 8.3e-12;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 72 TASLTISGLQAEDEADYYC 90
|||||||||||||||||||
Db 72 TASLTISGLQAEDEADYYC 90

RESULT 6
S36051
Ig lambda chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 21-Jan-2000
C;Accession: S36051
R;Williams, S.C.
submitted to the EMBL Data Library, April 1993
A;Reference number: S36046
A;Accession: S36051
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-99 <WIL>
A;Cross-references: EMBL:Z22192; NID:g312305; PIDN:CAA80202.1; PID:g312306
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-92/Domain: immunoglobulin homology <IMM>

Query Match 11.0%; Score 12; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 0.0001;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 79 GLQAEDEADYYC 90
||||||||||||
Db 79 GLQAEDEADYYC 90

RESULT 7
S36052
Ig lambda chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 21-Jan-2000
C;Accession: S36052
R;Williams, S.C.
submitted to the EMBL Data Library, April 1993
A;Reference number: S36046
A;Accession: S36052
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-99 <WIL>
A;Cross-references: EMBL:Z22193; NID:g312307; PIDN:CAA80203.1; PID:g312308
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-92/Domain: immunoglobulin homology <IMM>

Query Match 11.0%; Score 12; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 0.0001;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 79 GLQAEDEADYYC 90
||||||||||||
Db 79 GLQAEDEADYYC 90

RESULT 8
S36053
Ig lambda chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 21-Jan-2000
C;Accession: S36053
R;Williams, S.C.
submitted to the EMBL Data Library, April 1993
A;Reference number: S36046
A;Accession: S36053
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-99 <WIL>
A;Cross-references: EMBL:Z22194; NID:g312315; PIDN:CAA80204.1; PID:g312316
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-92/Domain: immunoglobulin homology <IMM>

Query Match 11.0%; Score 12; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 0.0001;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 79 GLQAEDEADYYC 90
||||||||||||
Db 79 GLQAEDEADYYC 90

RESULT 9
LIHUNM
Ig lambda chain V-I region (Newm) - human (tentative sequence)
C;Species: Homo sapiens (man)
C;Date: 23-Oct-1981 #sequence_revision 23-Oct-1981 #text_change 31-Mar-2000
C;Accession: A01968
R;Chen, B.L.; Poljak, R.J.
Biochemistry 13, 1295-1302, 1974
A;Title: Amino acid sequence of the (lambda) light chain of a human myeloma immunoglo
A;Reference number: A90375; MUID:74109253; PMID:4814727
A;Accession: A01968
A;Molecule type: protein
A;Residues: 1-103 <CHE>
A;Note: the absence of seven residues found in other lambda chains was confirmed by
A;Note: the C region of this chain has the Oz+ marker
R;Saul, F.A.; Amzel, L.M.; Poljak, R.J.
J. Biol. Chem. 253, 585-597, 1978
A;Title: Preliminary refinement and structural analysis of the fab fragment from hum
A;Reference number: A92235; MUID:78066916; PMID:618887
A;Contents: annotation; X-ray crystallography, 2.0 angstroms
A;Note: the structure of the Fab fragment of the IgGl myeloma protein Newm was determ
C;Genetics:
A;Gene: GDB:IGLV@
A;Cross-references: GDB:119342; OMIM:147240
A;Map position: 22q11.2-22q11.2
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate int
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: blocked amino end; heterotetramer
F;15-85/Domain: immunoglobulin homology <IMM>
F;1/Modified site: blocked amino end (Gln) (probably pyrrolidone carboxylic acid) #st
F;22-83/Disulfide bonds: #status predicted

Query Match 11.0%; Score 12; DB 1; Length 103;
Best Local Similarity 100.0%; Pred. No. 0.0001;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 79 GLQAEDEADYYC 90
||||||||||||
Db 72 GLQAEDEADYYC 83

RESULT 10
S42265
Ig kappa chain V region (018) - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 17-Mar-1999
C;Accession: S42265
R;Scott, M.G.; Crimmins, D.L.; McCourt, D.W.; Chung, G.; Schaeble, K.F.; Thiebe, R.;
J. Immunol. 147, 4007-4013, 1991
A;Title: Clonal characterization of the human IgG antibody repertoire to Haemophilus
A;Reference number: S42263; MUID:92043792; PMID:1940382
A;Accession: S42265
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-62 <SCO>
A;Cross-references: EMBL:M64856
C;Genetics:
A;Introns: 19/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 10.1%; Score 11; DB 2; Length 62;
Best Local Similarity 100.0%; Pred. No. 0.00071;

```
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         42 PGKAPKLLIYD 52
              |||||||||||
Db         40 PGKAPKLLIYD 50


RESULT 11
I52592
Ig kappa chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jan-2000
C;Accession: I52592
R;Wagner, S.D.; Martinelli, V.; Luzzatto, L.
Blood 83, 3647-3653, 1994
A;Title: Similar patterns of V kappa gene usage but different degrees of somatic mutatio
A;Reference number: I52592; MUID:94264318; PMID:8204889
A;Accession: I52592
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-87 <RES>
A;Cross-references: GB:S71057; NID:g547053; PIDN:AAB30971.1; PID:g547054
C;Genetics:
A;Gene: IgKV
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;9-83/Domain: immunoglobulin homology <IMM>

  Query Match           10.1%;  Score 11;  DB 2;  Length 87;
  Best Local Similarity  100.0%;  Pred. No. 0.00094;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         42 PGKAPKLLIYD 52
              |||||||||||
Db         33 PGKAPKLLIYD 43


RESULT 12
S34088
Ig kappa chain V region - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C;Accession: S34088
R;Wagner, S.D.; Luzzatto, L.
Eur. J. Immunol. 23, 391-397, 1993
A;Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distribute
A;Reference number: S34076; MUID:93170387; PMID:8436174
A;Accession: S34088
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-88 <WAG>
A;Cross-references: EMBL:X67172
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;9-83/Domain: immunoglobulin homology <IMM>

  Query Match           10.1%;  Score 11;  DB 2;  Length 88;
  Best Local Similarity  100.0%;  Pred. No. 0.00095;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         42 PGKAPKLLIYD 52
              |||||||||||
Db         33 PGKAPKLLIYD 43


RESULT 13
S34087
Ig kappa chain V region - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C;Accession: S34087
R;Wagner, S.D.; Luzzatto, L.
Eur. J. Immunol. 23, 391-397, 1993
A;Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distribute
A;Reference number: S34076; MUID:93170387; PMID:8436174
A;Accession: S34087
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-88 <WAG>
A;Cross-references: EMBL:X67171
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;9-83/Domain: immunoglobulin homology <IMM>

  Query Match           10.1%;  Score 11;  DB 2;  Length 88;
  Best Local Similarity  100.0%;  Pred. No. 0.00095;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         42 PGKAPKLLIYD 52
              |||||||||||
Db         33 PGKAPKLLIYD 43


RESULT 14
PH0862
Ig kappa chain V region (anti-DNA, III-3R) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 21-Jan-2000
C;Accession: PH0862
R;Manheimer-Lory, A.; Katz, J.B.; Pillinger, M.; Ghossein, C.; Smith, A.; Diamond, B
J. Exp. Med. 174, 1639-1652, 1991
A;Title: Molecular characteristics of antibodies bearing an anti-DNA-associated idio
A;Reference number: PH0862; MUID:92078875; PMID:1660528
A;Accession: PH0862
A;Molecule type: DNA
A;Residues: 1-95 <MAN>
C;Comment: This antibody is produced by Epstein-Barr virus-transformed B cell that h
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-23/Region: framework 1
F;16-90/Domain: immunoglobulin homology <IMM>
F;24-34/Region: complementarity-determining 1
F;35-49/Region: framework 2
F;50-56/Region: complementarity-determining 2
F;57-88/Region: framework 3
F;89-95/Region: complementarity-determining 3

  Query Match           10.1%;  Score 11;  DB 2;  Length 95;
  Best Local Similarity  100.0%;  Pred. No. 0.001;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         42 PGKAPKLLIYD 52
              |||||||||||
Db         40 PGKAPKLLIYD 50


RESULT 15
PH0864
Ig kappa chain V region (anti-DNA, IC4) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 21-Jan-2000
C;Accession: PH0864
R;Manheimer-Lory, A.; Katz, J.B.; Pillinger, M.; Ghossein, C.; Smith, A.; Diamond, B
J. Exp. Med. 174, 1639-1652, 1991
A;Title: Molecular characteristics of antibodies bearing an anti-DNA-associated idio
A;Reference number: PH0862; MUID:92078875; PMID:1660528
A;Accession: PH0864
A;Molecule type: DNA
A;Residues: 1-95 <MAN>
C;Comment: This antibody is produced by Epstein-Barr virus-transformed B cell that h
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-23/Region: framework 1
F;16-90/Domain: immunoglobulin homology <IMM>
F;24-34/Region: complementarity-determining 1
F;35-49/Region: framework 2
F;50-56/Region: complementarity-determining 2
```

F;57-88/Region: framework 3
F;89-95/Region: complementarity-determining 3

  Query Match 10.1%; Score 11; DB 2; Length 95;
  Best Local Similarity 100.0%; Pred. No. 0.001;
  Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 42 PGKAPKLLIYD 52
  |||||||||||
Db 40 PGKAPKLLIYD 50

RESULT 16
B46516
Ig lambda chain V region - horse (fragment)
C;Species: Equus caballus (domestic horse)
C;Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C;Accession: B46516
R;Home, W.A.; Ford, J.E.; Gibson, D.M.
J. Immunol. 149, 3927-3936, 1992
A;Title: L chain isotype regulation in horse. I. Characterization of Ig lambda genes.
A;Reference number: A46516; MUID:93094587; PMID:1460283
A;Accession: B46516
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-107 <HOM>
A;Experimental source: spleen
A;Note: sequence extracted from NCBI backbone (NCBIP:120369)
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;23-101/Domain: immunoglobulin homology <IMM>

  Query Match 10.1%; Score 11; DB 2; Length 107;
  Best Local Similarity 100.0%; Pred. No. 0.0011;
  Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 81 QAEDBADYYCS 91
  |||||||||||
Db 90 QAEDBADYYCS 100

RESULT 17
KIHUAU
Ig kappa chain V-I region (Au) - human
C;Species: Homo sapiens (man)
C;Date: 24-Apr-1984 #sequence_revision 02-Jul-1998 #text_change 21-Jan-2000
C;Accession: A91653; A01862; S02573
R;Schiechl, H.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 353, 345-370, 1972
A;Title: Die Primärstruktur einer monoklonalen Immunglobulin-L-Kette vom kappa-Typ, Sub
A;Reference number: A91653; MUID:72189444; PMID:5028201
A;Accession: A91653
A;Molecule type: protein
A;Residues: 1-108 <SCH>
A;Note: the C region of this chain has the Inv (3) marker
R;Fehlhammer, H.; Schiffer, M.; Epp, O.; Colman, P.M.; Lattman, E.E.; Schwager, P.; Steil
Biophys. Struct. Mech. 1, 139-146, 1975
A;Title: The structure determination of the variable portion of the Bence-Jones protein
A;Reference number: A90729; MUID:77022433; PMID:1234024
A;Contents: annotation; X-ray crystallography
A;Note: the structure of the V region was determined by molecular replacement methods us
R;Steiner, V.; Chang, J.Y.
FEBS Lett. 222, 6-10, 1987
A;Title: Chemical modification of the carboxyl groups of protein substrates enhances the
A;Reference number: S02572; MUID:88005152; PMID:3115831
A;Contents: annotation
C;Comment: This is a Bence Jones protein.
C;Genetics:
A;Gene: GDB:IGKV1
A;Cross-references: GDB:136264
A;Map position: 2p12-2p12
C;Complex: an immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds; in some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>
F;23-88/Disulfide bonds: #status predicted

  Query Match 10.1%; Score 11; DB 1; Length 108;
  Best Local Similarity 100.0%; Pred. No. 0.0011;
  Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 42 PGKAPKLLIYD 52
  |||||||||||
Db 40 PGKAPKLLIYD 50

RESULT 18
KIHURY
Ig kappa chain V-I region (Roy) - human (tentative sequence)
C;Species: Homo sapiens (man)
C;Date: 24-Apr-1984 #sequence_revision 02-Jul-1998 #text_change 31-Mar-2000
C;Accession: A91638; B94417; A01874; S02575
R;Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 348, 1077-1080, 1967
A;Title: Die chemische Struktur von zwei Bence-Jones-Proteinen (Roy und Cum.) vom kap
A;Reference number: A91638; MUID:68362076; PMID:5595110
A;Accession: A91638
A;Molecule type: protein
A;Residues: 1-38,'GPK',42-108 <HIL>
A;Note: the sequence of the C region, which has the Inv (1,2) marker, is also given
R;Hilschmann, N.; Barnikol, H.U.; Hess, M.; Langer, B.; Ponstingl, H.; Steinmetz-Kayn
in Gamma Globulins: Structure and Function, Franek, F., and Shugar, D., eds., pp.57-
A;Reference number: A94417
A;Contents: revisions to residues 39 and 41
A;Accession: B94417
A;Molecule type: protein
A;Residues: 39;41 <HI2>
R;Steiner, V., Chang, J.Y.
FEBS Lett. 222, 6-10, 1987
A;Title: Chemical modification of the carboxyl groups of protein substrates enhances
A;Reference number: S02572; MUID:88005152; PMID:3115831
A;Contents: annotation
C;Comment: This is a Bence Jones protein.
C;Genetics:
A;Gene: GDB:IGKV1
A;Cross-references: GDB:136264
A;Map position: 2p12-2p12
C;Complex: an immunoglobulin heterotetramer subunit consists of two identical light (
hain disulfide bonds; in some cases, such as IgA and IgM, the subunits associate into
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>
F;23-88/Disulfide bonds: #status predicted

  Query Match 10.1%; Score 11; DB 1; Length 108;
  Best Local Similarity 100.0%; Pred. No. 0.0011;
  Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 42 PGKAPKLLIYD 52
  |||||||||||
Db 40 PGKAPKLLIYD 50

RESULT 19
PH0881
Ig kappa chain V region (GOU) - human (fragment)
N;Alternate names: myeloma protein
C;Species: Homo sapiens (man)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 09-May-1997
C;Accession: PH0881
R;Manheimer-Lory, A.; Katz, J.B.; Pillinger, M.; Ghossein, C.; Smith, A.; Diamond, B.
J. Exp. Med. 174, 1639-1652, 1991
A;Title: Molecular characteristics of antibodies bearing an anti-DNA-associated idiot
A;Reference number: PH0862; MUID:92078875; PMID:1660528
A;Accession: PH0881
A;Molecule type: protein

```
A;Residues: 1-53 <MAN>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-23/Region: framework 1
F;24-34/Region: complementarity-determining 1
F;35-49/Region: framework 2
F;50-53/Region: complementarity-determining 2

  Query Match             9.2%;  Score 10;  DB 2;  Length 53;
  Best Local Similarity   100.0%;  Pred. No. 0.0065;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          42 PGKAPKLLIY 51
               ||||||||||
Db          40 PGKAPKLLIY 49


RESULT 20
A24626
Ig lambda chain V-II region (Har) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 25-Oct-1987 #sequence_revision 25-Oct-1987 #text_change 16-Aug-1996
C;Accession: A24626
R;Hulitz, M.; Lilke, R.
Biol. Chem. Hoppe-Seyler 366; 907-915, 1985
A;Title: Amyloid fibrils derived from V-region together with C-region fragments from a l
A;Reference number: A24626; MUID:86077295; PMID:3935132
A;Accession: A24626
A;Molecule type: protein
A;Residues: 1-60 <EUL>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

  Query Match             9.2%;  Score 10;  DB 2;  Length 60;
  Best Local Similarity   100.0%;  Pred. No. 0.0072;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 ASVSGSPGQS 17
              ||||||||||
Db          1 ASVSGSPGQS 10


RESULT 21
PH0880
Ig kappa chain V region (SCH) - human (fragment)
N;Alternate names: myeloma protein
C;Species: Homo sapiens (man)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 09-May-1997
C;Accession: PH0880
R;Manheimer-Lory, A.; Katz, J.B.; Pillinger, M.; Ghossein, C.; Smith, A.; Diamond, B.
J. Exp. Med. 174, 1639-1652, 1991
A;Title: Molecular characteristics of antibodies bearing an anti-DNA-associated idiotype
A;Reference number: PH0862; MUID:92078875; PMID:1660528
A;Accession: PH0880
A;Molecule type: protein
A;Residues: 1-65 <MAN>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-23/Region: framework 1
F;24-34/Region: complementarity-determining 1
F;35-49/Region: framework 2
F;50-56/Region: complementarity-determining 2
F;57-65/Region: framework 3

  Query Match             9.2%;  Score 10;  DB 2;  Length 65;
  Best Local Similarity   100.0%;  Pred. No. 0.0077;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          42 PGKAPKLLIY 51
               ||||||||||
Db          40 PGKAPKLLIY 49


RESULT 22
S34090
Ig kappa chain V region - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C;Accession: S34090
R;Wagner, S.D.; Luzzatto, L.
Eur. J. Immunol. 23, 391-397, 1993
A;Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distri
A;Reference number: S34076; MUID:93170387; PMID:8436174
A;Accession: S34090
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-82 <WAG>
A;Cross-references: EMBL:X67174
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;7-81/Domain: immunoglobulin homology <IMM>

  Query Match             9.2%;  Score 10;  DB 2;  Length 82;
  Best Local Similarity   100.0%;  Pred. No. 0.0093;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          42 PGKAPKLLIY 51
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Db          31 PGKAPKLLIY 40


RESULT 23
S34086
Ig kappa chain V region - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C;Accession: S34086
R;Wagner, S.D.; Luzzatto, L.
Eur. J. Immunol. 23, 391-397, 1993
A;Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distri
A;Reference number: S34076; MUID:93170387; PMID:8436174
A;Accession: S34086
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-86 <WAG>
A;Cross-references: EMBL:X67169
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;9-83/Domain: immunoglobulin homology <IMM>

  Query Match             9.2%;  Score 10;  DB 2;  Length 86;
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  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          42 PGKAPKLLIY 51
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Db          33 PGKAPKLLIY 42


RESULT 24
S16840
Ig kappa chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 10-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Accession: S16840
R;Blaison, G.; Kuntz, J.L.; Pasquali, J.L.
Eur. J. Immunol. 21, 1221-1227, 1991
A;Title: Molecular analysis of V(kappa)III variable regions of polyclonal rheumatoid
A;Reference number: S16823; MUID:91243737; PMID:1903706
A;Accession: S16840
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-86 <BLA>
A;Cross-references: EMBL:X54838
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
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F;7-81/Domain: immunoglobulin homology <IMM>

Query Match 9.2%; Score 10; DB 2; Length 86;
Best Local Similarity 100.0%; Pred. No. 0.0097;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 42 PGKAPKLLIY 51
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Db 31 PGKAPKLLIY 40

RESULT 25
S21523
Ig kappa chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 20-Feb-1995 #sequence_revision 25-Oct-1996 #text_change 21-Jan-2000
C;Accession: S34079; S21523
R;Wagner, S.D.; Luzzatto, L.
Eur. J. Immunol. 23, 391-397, 1993
A;Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distribute
A;Reference number: S34076; MUID:93170387; PMID:8436174
A;Accession: S34079
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-87 <WA2>
A;Cross-references: EMBL:X66039; NID:g33312; PIDN:CAA46838.1; PID:g33313
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;9-83/Domain: immunoglobulin homology <IMM>

Query Match 9.2%; Score 10; DB 2; Length 87;
Best Local Similarity 100.0%; Pred. No. 0.0098;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 42 PGKAPKLLIY 51
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Db 33 PGKAPKLLIY 42

Search completed: March 15, 2004, 07:43:56
Job time : 21 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: March 15, 2004, 07:42:10 ; Search time 34 Seconds
(without alignments)
676.933 Million cell updates/sec

Title: US-09-620-955B-4
Perfect score: 109
Sequence: 1 QSALTQPASVSGSPQGSITI.....CSSFANSGPLPGGGTKVTVL 109

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 809742 seqs, 211153259 residues

Word size : 0

Total number of hits satisfying chosen parameters: 332758

Minimum DB seq length: 0
Maximum DB seq length: 109

Post-processing: Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	28	25.7	90	14	US-10-125-687-27	Sequence 27, Appl
2	28	25.7	99	15	US-10-308-817-99	Sequence 99, Appl
3	28	25.7	99	15	US-10-308-817-101	Sequence 101, App
4	26	23.9	104	14	US-10-127-893-153	Sequence 153, App
5	26	23.9	104	15	US-10-340-189-17	Sequence 17, Appl
6	26	23.9	104	15	US-10-325-696-17	Sequence 17, Appl
7	23	21.1	103	14	US-10-026-925-98	Sequence 98, Appl
8	22	20.2	22	10	US-09-563-222-94	Sequence 94, Appl
9	21	19.3	50	9	US-09-863-693-14	Sequence 14, Appl
10	21	19.3	50	9	US-09-863-693-15	Sequence 15, Appl
11	21	19.3	50	9	US-09-863-693-16	Sequence 16, Appl
12	21	19.3	50	9	US-09-863-693-17	Sequence 17, Appl
13	21	19.3	50	9	US-09-863-693-18	Sequence 18, Appl
14	21	19.3	50	9	US-09-863-693-19	Sequence 19, Appl
15	21	19.3	50	9	US-09-863-693-20	Sequence 20, Appl
16	21	19.3	50	9	US-09-863-693-21	Sequence 21, Appl
17	21	19.3	50	9	US-09-863-693-22	Sequence 22, Appl
18	21	19.3	50	11	US-09-373-403-14	Sequence 14, Appl
19	21	19.3	50	11	US-09-373-403-15	Sequence 15, Appl
20	21	19.3	50	11	US-09-373-403-16	Sequence 16, Appl
21	21	19.3	50	11	US-09-373-403-17	Sequence 17, Appl
22	21	19.3	50	11	US-09-373-403-18	Sequence 18, Appl
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27	21	19.3	50	14	US-10-143-437-14	Sequence 14, Appl
28	21	19.3	50	14	US-10-143-437-15	Sequence 15, Appl
29	21	19.3	50	14	US-10-143-437-16	Sequence 16, Appl
30	21	19.3	50	14	US-10-143-437-17	Sequence 17, Appl
31	21	19.3	50	14	US-10-143-437-18	Sequence 18, Appl
32	21	19.3	50	14	US-10-143-437-19	Sequence 19, Appl
33	21	19.3	50	14	US-10-143-437-20	Sequence 20, Appl
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51	12	11.0	103	15	US-10-325-696-3	Sequence 3, Appli
52	12	11.0	104	10	US-09-848-798-49	Sequence 49, Appl
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58	11	10.1	90	9	US-09-864-761-34739	Sequence 34739, A
59	11	10.1	95	9	US-09-158-120A-19	Sequence 19, Appl
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61	11	10.1	95	14	US-10-194-975-56	Sequence 56, Appl
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64	11	10.1	95	14	US-10-194-975-64	Sequence 64, Appl
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81	11	10.1	106	9	US-09-771-415-17	Sequence 17, Appl
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84	11	10.1	106	9	US-09-771-415-23	Sequence 23, Appl
85	11	10.1	106	9	US-09-771-415-25	Sequence 25, Appl
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87	11	10.1	106	9	US-09-996-288-11	Sequence 11, Appl
88	11	10.1	106	9	US-09-996-288-13	Sequence 13, Appl

89	11	10.1	106	9	US-09-996-288-21	Sequence 21, Appl
90	11	10.1	106	9	US-09-996-288-26	Sequence 26, Appl
91	11	10.1	106	9	US-09-996-288-30	Sequence 30, Appl
92	11	10.1	106	9	US-09-996-288-34	Sequence 34, Appl
93	11	10.1	106	9	US-09-996-288-38	Sequence 38, Appl
94	11	10.1	106	9	US-09-996-288-42	Sequence 42, Appl
95	11	10.1	106	9	US-09-996-288-46	Sequence 46, Appl
96	11	10.1	106	9	US-09-996-288-49	Sequence 49, Appl
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ALIGNMENTS

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RESULT 1
US-10-125-687-27
; Sequence 27, Application US/10125687
; Publication No. US20030054407A1
; GENERAL INFORMATION:
;  APPLICANT: Luo, Peter
;  TITLE OF INVENTION: STRUCTURE-BASED CONSTRUCTION OF HUMAN ANTIBODY LIBRARY
;  FILE REFERENCE: 26050-705
;  CURRENT APPLICATION NUMBER: US/10/125,687
;  CURRENT FILING DATE:  2002-04-17
;  NUMBER OF SEQ ID NOS: 28
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
;    LENGTH: 90
;    TYPE: PRT
;    ORGANISM: Homo sapiens
US-10-125-687-27

  Query Match             25.7%;  Score 28;  DB 14;  Length 90;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-19;
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Qy          1 QSALTQPASVSGSPGQSITISCTGTSSD 28
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Db          1 QSALTQPASVSGSPGQSITISCTGTSSD 28


RESULT 2
US-10-308-817-99
; Sequence 99, Application US/10308817
; Publication No. US20030219861A1
; GENERAL INFORMATION:
;  APPLICANT: Rother, Russell
;  APPLICANT:  Wu, Dayang
;  TITLE OF INVENTION: HYBRID ANTIBODIES
;  FILE REFERENCE: 1087-37
;  CURRENT APPLICATION NUMBER: US/10/308,817
;  CURRENT FILING DATE:  2002-12-03
;  NUMBER OF SEQ ID NOS: 195
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 99
;    LENGTH: 99
;    TYPE: PRT
;    ORGANISM: human
US-10-308-817-99

  Query Match             25.7%;  Score 28;  DB 15;  Length 99;
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  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db          1 QSALTQPASVSGSPGQSITISCTGTSSD 28


RESULT 3
US-10-308-817-101
; Sequence 101, Application US/10308817
; Publication No. US20030219861A1
; GENERAL INFORMATION:
;  APPLICANT: Rother, Russell
;  APPLICANT:  Wu, Dayang
;  TITLE OF INVENTION: HYBRID ANTIBODIES
;  FILE REFERENCE: 1087-37
;  CURRENT APPLICATION NUMBER: US/10/308,817
;  CURRENT FILING DATE:  2002-12-03
;  NUMBER OF SEQ ID NOS: 195
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 101
;    LENGTH: 99
;    TYPE: PRT
;    ORGANISM: human
US-10-308-817-101

  Query Match             25.7%;  Score 28;  DB 15;  Length 99;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-19;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db          1 QSALTQPASVSGSPGQSITISCTGTSSD 28


RESULT 4
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; Publication No. US20030166196A1
;  GENERAL INFORMATION:
;       APPLICANT: Better, Marc D.
;                  Carroll, Stephen F.
;                  Studnika, Gary M.
;       TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
;                           Proteins
;       NUMBER OF SEQUENCES: 173
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: McAndrews, Held & Malloy, Ltd.
;            STREET: 500 West Madison Street, 34th floor
;            CITY: Chicago
;            STATE: Illinois
;            COUNTRY: USA
;            ZIP: 60661
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/127,890
;            FILING DATE: 23-Apr-2002
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/08/646,360
;            FILING DATE: 13-MAY-1996
;            APPLICATION NUMBER: PCT/US94/05348
;            FILING DATE: 12-MAY-1994
;            APPLICATION NUMBER: US 08/064,691
;            FILING DATE: 12-MAY-1993
;            APPLICATION NUMBER: US 07/988,430
;            FILING DATE: 09-DEC-1992
;            APPLICATION NUMBER: US 07/901,707
;            FILING DATE: 19-JUN-1992
;            APPLICATION NUMBER: US 07/787,567
;            FILING DATE: 04-NOV-1991
;       ATTORNEY/AGENT INFORMATION:
;            NAME: McNicholas, Janet M.
;            REGISTRATION NUMBER: 32,918
;            REFERENCE/DOCKET NUMBER: 200-70.P4
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 312/707-8889
```

; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 153:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 104 amino acids
; TYPE: amino acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 153:
US-10-127-890-153

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Best Local Similarity 100.0%; Pred. No. 2.1e-17;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 2 SALTQPASVSGSPGQSITISCTGTSS 27

RESULT 5
US-10-340-189-17
; Sequence 17, Application US/10340189
; Publication No. US20030229207A1
; GENERAL INFORMATION:
; APPLICANT: Studnicka, Gary M.
; TITLE OF INVENTION: Modified Antibody Variable Domains
; NUMBER OF SEQUENCES: 89
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 W. Madison Street, 34th Floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/340,189
; FILING DATE: 10-Jan-2003
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/245,202A
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/082,842
; FILING DATE: 23-JUN-1993
; APPLICATION NUMBER: PCT/US92/10906
; FILING DATE: 14-DEC-1992
; APPLICATION NUMBER: US 07/808,464
; FILING DATE: 13-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11023US07 / 200-71.P2.C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 104 amino acids
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
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US-10-340-189-17

Query Match 23.9%; Score 26; DB 15; Length 104;
Best Local Similarity 100.0%; Pred. No. 2.1e-17;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 6
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; Sequence 17, Application US/10325696
; Publication No. US20040005630A1
; GENERAL INFORMATION:
; APPLICANT: Studnicka, Gary M.
; TITLE OF INVENTION: Modified Antibody Variable Domains
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th Floor
; CITY: Chicago
; STATE: IL
; COUNTRY: United States of America
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/325,696
; FILING DATE: 18-Dec-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/097,980
; FILING DATE: 16-JUN-1998
; APPLICATION NUMBER: 08/107,669
; FILING DATE: 13-AUG-1993
; APPLICATION NUMBER: PCT/US92/10906
; FILING DATE: 14-DEC-1992
; APPLICATION NUMBER: US 07/808,464
; FILING DATE: 13-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Janet M. McNicholas, Ph.D.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11023US06/200-71.P1.C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9050
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 104 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-10-325-696-17

Query Match 23.9%; Score 26; DB 15; Length 104;
Best Local Similarity 100.0%; Pred. No. 2.1e-17;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SALTQPASVSGSPGQSITISCTGTSS 27
||||||||||||||||||||||||||
Db 2 SALTQPASVSGSPGQSITISCTGTSS 27

RESULT 7
US-10-026-925-98
; Sequence 98, Application US/10026925
; Publication No. US20030119056A1
; GENERAL INFORMATION:
; APPLICANT: LADNER, ROBERT C.
; TITLE OF INVENTION: FOCUSED LIBRARIES OF GENETIC PACKAGES
; FILE REFERENCE: DYAX/004

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;  CURRENT APPLICATION NUMBER: US/10/026,925
;  CURRENT FILING DATE:  2002-05-28
;  NUMBER OF SEQ ID NOS: 99
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 98
;    LENGTH: 103
;    TYPE: PRT
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Description of Artificial Sequence: 2a2: JH2 Human
;    OTHER INFORMATION: lambda-chain gene with stuffers in place of CDRs
US-10-026-925-98

  Query Match             21.1%;  Score 23;  DB 14;  Length 103;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-14;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QSALTQPASVSGSPGQSITISCT 23
              |||||||||||||||||||||||
Db          3 QSALTQPASVSGSPGQSITISCT 25


RESULT 8
US-09-563-222-94
; Sequence 94, Application US/09563222
; Publication No. US20030079253A1
; GENERAL INFORMATION:
;  APPLICANT:  Hiatt, Andrew
;  APPLICANT:  Hein, Mich B.
;  TITLE OF INVENTION:  IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN
;  TITLE OF INVENTION:  EUKARYOTIC CELLS
;  FILE REFERENCE:  310098.406
;  CURRENT APPLICATION NUMBER: US/09/563,222
;  CURRENT FILING DATE:  2000-05-02
;  NUMBER OF SEQ ID NOS:  197
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 94
;    LENGTH: 22
;    TYPE: PRT
;    ORGANISM: Homo sapien
US-09-563-222-94

  Query Match             20.2%;  Score 22;  DB 10;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 4.1e-14;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QSALTQPASVSGSPGQSITISC 22
              ||||||||||||||||||||||
Db          1 QSALTQPASVSGSPGQSITISC 22


RESULT 9
US-09-863-693-14
; Sequence 14, Application US/09863693
; Patent No. US20020062010A1
;   GENERAL INFORMATION:
;        APPLICANT: ARATHOON, R.
;                   CARTER, P.J.
;                   MERCHANT, A.M.
;                   PRESTA, L.G.
;        TITLE OF INVENTION: METHOD FOR MAKING MULTISPECIFIC ANTIBODIES
;                            HAVING HETEROMULTIMERIC AND COMMON COMPONENTS
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Genentech, Inc.
;             STREET: 1 DNA Way
;             CITY: South San Francisco
;             STATE: California
;             COUNTRY: USA
;             ZIP: 94080
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: WinPatin (Genentech)
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/863,693
;             FILING DATE: 23-May-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/070,166
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Conley, Deirdre L.
;             REGISTRATION NUMBER: 36,487
;             REFERENCE/DOCKET NUMBER: P1099R1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 650/225-2066
;             TELEFAX: 650/952-9881
;   INFORMATION FOR SEQ ID NO: 14:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 50 amino acids
;             TYPE: Amino Acid
;             TOPOLOGY: Linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-863-693-14

  Query Match             19.3%;  Score 21;  DB 9;  Length 50;
  Best Local Similarity   100.0%;  Pred. No. 7.6e-13;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         72 TASLTSGLQAEDEADYYCSS 92
              |||||||||||||||||||||
Db         12 TASLTSGLQAEDEADYYCSS 32


RESULT 10
US-09-863-693-15
; Sequence 15, Application US/09863693
; Patent No. US20020062010A1
;   GENERAL INFORMATION:
;        APPLICANT: ARATHOON, R.
;                   CARTER, P.J.
;                   MERCHANT, A.M.
;                   PRESTA, L.G.
;        TITLE OF INVENTION: METHOD FOR MAKING MULTISPECIFIC ANTIBODIES
;                            HAVING HETEROMULTIMERIC AND COMMON COMPONENTS
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Genentech, Inc.
;             STREET: 1 DNA Way
;             CITY: South San Francisco
;             STATE: California
;             COUNTRY: USA
;             ZIP: 94080
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: WinPatin (Genentech)
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/863,693
;             FILING DATE: 23-May-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/070,166
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Conley, Deirdre L.
;             REGISTRATION NUMBER: 36,487
;             REFERENCE/DOCKET NUMBER: P1099R1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 650/225-2066
;             TELEFAX: 650/952-9881
;   INFORMATION FOR SEQ ID NO: 15:
;        SEQUENCE CHARACTERISTICS:
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;              LENGTH: 50 amino acids
;              TYPE: Amino Acid
;              TOPOLOGY: Linear
;         SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-863-693-15

  Query Match              19.3%;  Score 21;  DB 9;  Length 50;
  Best Local Similarity   100.0%;  Pred. No. 7.6e-13;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          72 TASLTISGLQAEDEADYYCSS 92
               |||||||||||||||||||||
Db          12 TASLTISGLQAEDEADYYCSS 32


RESULT 11
US-09-863-693-16
; Sequence 16, Application US/09863693
; Patent No. US20020062010A1
;   GENERAL INFORMATION:
;        APPLICANT: ARATHOON, R.
;                   CARTER, P.J.
;                   MERCHANT, A.M.
;                   PRESTA, L.G.
;        TITLE OF INVENTION: METHOD FOR MAKING MULTISPECIFIC ANTIBODIES
;                            HAVING HETEROMULTIMERIC AND COMMON COMPONENTS
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Genentech, Inc.
;             STREET: 1 DNA Way
;             CITY: South San Francisco
;             STATE: California
;             COUNTRY: USA
;             ZIP: 94080
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: WinPatin (Genentech)
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/863,693
;             FILING DATE: 23-May-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/070,166
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Conley, Deirdre L.
;             REGISTRATION NUMBER: 36,487
;             REFERENCE/DOCKET NUMBER: P1099R1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 650/225-2066
;             TELEFAX: 650/952-9881
;   INFORMATION FOR SEQ ID NO: 16:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 50 amino acids
;             TYPE: Amino Acid
;             TOPOLOGY: Linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-863-693-16

  Query Match              19.3%;  Score 21;  DB 9;  Length 50;
  Best Local Similarity   100.0%;  Pred. No. 7.6e-13;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          72 TASLTISGLQAEDEADYYCSS 92
               |||||||||||||||||||||
Db          12 TASLTISGLQAEDEADYYCSS 32


RESULT 12
US-09-863-693-17
; Sequence 17, Application US/09863693
; Patent No. US20020062010A1
;   GENERAL INFORMATION:
;        APPLICANT: ARATHOON, R.
;                   CARTER, P.J.
;                   MERCHANT, A.M.
;                   PRESTA, L.G.
;        TITLE OF INVENTION: METHOD FOR MAKING MULTISPECIFIC ANTIBODIES
;                            HAVING HETEROMULTIMERIC AND COMMON COMPONENTS
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Genentech, Inc.
;             STREET: 1 DNA Way
;             CITY: South San Francisco
;             STATE: California
;             COUNTRY: USA
;             ZIP: 94080
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: WinPatin (Genentech)
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/863,693
;             FILING DATE: 23-May-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/070,166
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Conley, Deirdre L.
;             REGISTRATION NUMBER: 36,487
;             REFERENCE/DOCKET NUMBER: P1099R1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 650/225-2066
;             TELEFAX: 650/952-9881
;   INFORMATION FOR SEQ ID NO: 17:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 50 amino acids
;             TYPE: Amino Acid
;             TOPOLOGY: Linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-863-693-17

  Query Match              19.3%;  Score 21;  DB 9;  Length 50;
  Best Local Similarity   100.0%;  Pred. No. 7.6e-13;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          72 TASLTISGLQAEDEADYYCSS 92
               |||||||||||||||||||||
Db          12 TASLTISGLQAEDEADYYCSS 32


RESULT 13
US-09-863-693-18
; Sequence 18, Application US/09863693
; Patent No. US20020062010A1
;   GENERAL INFORMATION:
;        APPLICANT: ARATHOON, R.
;                   CARTER, P.J.
;                   MERCHANT, A.M.
;                   PRESTA, L.G.
;        TITLE OF INVENTION: METHOD FOR MAKING MULTISPECIFIC ANTIBODIES
;                            HAVING HETEROMULTIMERIC AND COMMON COMPONENTS
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Genentech, Inc.
;             STREET: 1 DNA Way
;             CITY: South San Francisco
;             STATE: California
;             COUNTRY: USA
;             ZIP: 94080
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
;
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/863,693
; FILING DATE: 23-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/070,166
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Conley, Deirdre L.
; REGISTRATION NUMBER: 36,487
; REFERENCE/DOCKET NUMBER: P1099R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-2066
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 50 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-863-693-18

Query Match 19.3%; Score 21; DB 9; Length 50;
Best Local Similarity 100.0%; Pred. No. 7.6e-13;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 72 TASLTISGLQAEDEADYYCSS 92
||||||||||||||||||||||
Db 12 TASLTISGLQAEDEADYYCSS 32

RESULT 14
US-09-863-693-19
; Sequence 19, Application US/09863693
; Patent No. US20020062010A1
; GENERAL INFORMATION:
; APPLICANT: ARATHOON, R.
; CARTER, P.J.
; MERCHANT, A.M.
; PRESTA, L.G.
; TITLE OF INVENTION: METHOD FOR MAKING MULTISPECIFIC ANTIBODIES
; HAVING HETEROMULTIMERIC AND COMMON COMPONENTS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/863,693
; FILING DATE: 23-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/070,166
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Conley, Deirdre L.
; REGISTRATION NUMBER: 36,487
; REFERENCE/DOCKET NUMBER: P1099R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-2066
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 50 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-863-693-19

Query Match 19.3%; Score 21; DB 9; Length 50;
Best Local Similarity 100.0%; Pred. No. 7.6e-13;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 72 TASLTISGLQAEDEADYYCSS 92
||||||||||||||||||||||
Db 12 TASLTISGLQAEDEADYYCSS 32

RESULT 15
US-09-863-693-20
; Sequence 20, Application US/09863693
; Patent No. US20020062010A1
; GENERAL INFORMATION:
; APPLICANT: ARATHOON, R.
; CARTER, P.J.
; MERCHANT, A.M.
; PRESTA, L.G.
; TITLE OF INVENTION: METHOD FOR MAKING MULTISPECIFIC ANTIBODIES
; HAVING HETEROMULTIMERIC AND COMMON COMPONENTS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/863,693
; FILING DATE: 23-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/070,166
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Conley, Deirdre L.
; REGISTRATION NUMBER: 36,487
; REFERENCE/DOCKET NUMBER: P1099R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-2066
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 50 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-09-863-693-20

Query Match 19.3%; Score 21; DB 9; Length 50;
Best Local Similarity 100.0%; Pred. No. 7.6e-13;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 72 TASLTISGLQAEDEADYYCSS 92
||||||||||||||||||||||
Db 12 TASLTISGLQAEDEADYYCSS 32

RESULT 16
US-09-863-693-21

```
; Sequence 21, Application US/09863693
; Patent No. US20020062010A1
;  GENERAL INFORMATION:
;       APPLICANT: ARATHOON, R.
;                  CARTER, P.J.
;                  MERCHANT, A.M.
;                  PRESTA, L.G.
;       TITLE OF INVENTION: METHOD FOR MAKING MULTISPECIFIC ANTIBODIES
;                           HAVING HETEROMULTIMERIC AND COMMON COMPONENTS
;       NUMBER OF SEQUENCES: 26
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Genentech, Inc.
;            STREET: 1 DNA Way
;            CITY: South San Francisco
;            STATE: California
;            COUNTRY: USA
;            ZIP: 94080
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: WinPatin (Genentech)
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/863,693
;            FILING DATE: 23-May-2001
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 09/070,166
;            FILING DATE: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Conley, Deirdre L.
;            REGISTRATION NUMBER: 36,487
;            REFERENCE/DOCKET NUMBER: P1099R1
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 650/225-2066
;            TELEFAX: 650/952-9881
;  INFORMATION FOR SEQ ID NO: 21:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 50 amino acids
;            TYPE: Amino Acid
;            TOPOLOGY: Linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-09-863-693-21

  Query Match             19.3%;  Score 21;  DB 9;  Length 50;
  Best Local Similarity   100.0%;  Pred. No. 7.6e-13;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          72 TASLTISGLQAEDEADYYCSS 92
               |||||||||||||||||||||
Db          12 TASLTISGLQAEDEADYYCSS 32


RESULT 17
US-09-863-693-22
; Sequence 22, Application US/09863693
; Patent No. US20020062010A1
;  GENERAL INFORMATION:
;       APPLICANT: ARATHOON, R.
;                  CARTER, P.J.
;                  MERCHANT, A.M.
;                  PRESTA, L.G.
;       TITLE OF INVENTION: METHOD FOR MAKING MULTISPECIFIC ANTIBODIES
;                           HAVING HETEROMULTIMERIC AND COMMON COMPONENTS
;       NUMBER OF SEQUENCES: 26
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Genentech, Inc.
;            STREET: 1 DNA Way
;            CITY: South San Francisco
;            STATE: California
;            COUNTRY: USA
;            ZIP: 94080
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: WinPatin (Genentech)
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/863,693
;            FILING DATE: 23-May-2001
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 09/070,166
;            FILING DATE: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Conley, Deirdre L.
;            REGISTRATION NUMBER: 36,487
;            REFERENCE/DOCKET NUMBER: P1099R1
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 650/225-2066
;            TELEFAX: 650/952-9881
;  INFORMATION FOR SEQ ID NO: 22:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 50 amino acids
;            TYPE: Amino Acid
;            TOPOLOGY: Linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-863-693-22

  Query Match             19.3%;  Score 21;  DB 9;  Length 50;
  Best Local Similarity   100.0%;  Pred. No. 7.6e-13;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          72 TASLTISGLQAEDEADYYCSS 92
               |||||||||||||||||||||
Db          12 TASLTISGLQAEDEADYYCSS 32


RESULT 18
US-09-373-403-14
; Sequence 14, Application US/09373403
; Publication No. US20030207346A1
; GENERAL INFORMATION:
;  APPLICANT: ARATHOON, W. R.
;  APPLICANT:  CARTER, P.J.
;  APPLICANT:  MERCHANT, A.M.
;  APPLICANT:  PRESTA, L.G.
;  TITLE OF INVENTION: METHOD FOR MAKING MULTISPECIFIC ANTIBODIES HAVING
;  TITLE OF INVENTION:  HETEROMULTIMERIC AND COMMON COMPONENTS
;  FILE REFERENCE: P1099C1 a
;  CURRENT APPLICATION NUMBER: US/09/373,403
;  CURRENT FILING DATE:  1999-08-12
;  PRIOR APPLICATION NUMBER: US 08/850,058
;  PRIOR FILING DATE: 1997-05-02
;  NUMBER OF SEQ ID NOS: 26
; SEQ ID NO 14
;   LENGTH: 50
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Recombinant
US-09-373-403-14

  Query Match             19.3%;  Score 21;  DB 11;  Length 50;
  Best Local Similarity   100.0%;  Pred. No. 7.6e-13;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          72 TASLTISGLQAEDEADYYCSS 92
               |||||||||||||||||||||
Db          12 TASLTISGLQAEDEADYYCSS 32


RESULT 19
US-09-373-403-15
; Sequence 15, Application US/09373403
; Publication No. US20030207346A1
```

; GENERAL INFORMATION:
; APPLICANT: ARATHOON, W. R.
; APPLICANT: CARTER, P.J.
; APPLICANT: MERCHANT, A.M.
; APPLICANT: PRESTA, L.G.
; TITLE OF INVENTION: METHOD FOR MAKING MULTISPECIFIC ANTIBODIES HAVING
; TITLE OF INVENTION: 'HETEROMULTIMERIC AND COMMON COMPONENTS
; FILE REFERENCE: P1099C1 a
; CURRENT APPLICATION NUMBER: US/09/373,403
; CURRENT FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: US 08/850,058
; PRIOR FILING DATE: 1997-05-02
; NUMBER OF SEQ ID NOS: 26
; SEQ ID NO 15
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Recombinant
US-09-373-403-15

Query Match 19.3%; Score 21; DB 11; Length 50;
Best Local Similarity 100.0%; Pred. No. 7.6e-13;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 72 TASLTISGLQAEDEADYYCSS 92
||||||||||||||||||||||
Db 12 TASLTISGLQAEDEADYYCSS 32

RESULT 20
US-09-373-403-16
; Sequence 16, Application US/09373403
; Publication No. US20030207346A1
; GENERAL INFORMATION:
; APPLICANT: ARATHOON, W. R.
; APPLICANT: CARTER, P.J.
; APPLICANT: MERCHANT, A.M.
; APPLICANT: PRESTA, L.G.
; TITLE OF INVENTION: METHOD FOR MAKING MULTISPECIFIC ANTIBODIES HAVING
; TITLE OF INVENTION: HETEROMULTIMERIC AND COMMON COMPONENTS
; FILE REFERENCE: P1099C1 a
; CURRENT APPLICATION NUMBER: US/09/373,403
; CURRENT FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: US 08/850,058
; PRIOR FILING DATE: 1997-05-02
; NUMBER OF SEQ ID NOS: 26
; SEQ ID NO 16
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Recombinant
US-09-373-403-16

Query Match 19.3%; Score 21; DB 11; Length 50;
Best Local Similarity 100.0%; Pred. No. 7.6e-13;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 72 TASLTISGLQAEDEADYYCSS 92
||||||||||||||||||||||
Db 12 TASLTISGLQAEDEADYYCSS 32

RESULT 21
US-09-373-403-17
; Sequence 17, Application US/09373403
; Publication No. US20030207346A1
; GENERAL INFORMATION:
; APPLICANT: ARATHOON, W. R.
; APPLICANT: CARTER, P.J.
; APPLICANT: MERCHANT, A.M.
; APPLICANT: PRESTA, L.G.
; TITLE OF INVENTION: METHOD FOR MAKING MULTISPECIFIC ANTIBODIES HAVING
; TITLE OF INVENTION: HETEROMULTIMERIC AND COMMON COMPONENTS
; FILE REFERENCE: P1099C1 a
; CURRENT APPLICATION NUMBER: US/09/373,403
; CURRENT FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: US 08/850,058
; PRIOR FILING DATE: 1997-05-02
; NUMBER OF SEQ ID NOS: 26
; SEQ ID NO 17
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Recombinant
US-09-373-403-17

Query Match 19.3%; Score 21; DB 11; Length 50;
Best Local Similarity 100.0%; Pred. No. 7.6e-13;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 72 TASLTISGLQAEDEADYYCSS 92
||||||||||||||||||||||
Db 12 TASLTISGLQAEDEADYYCSS 32

RESULT 22
US-09-373-403-18
; Sequence 18, Application US/09373403
; Publication No. US20030207346A1
; GENERAL INFORMATION:
; APPLICANT: ARATHOON, W. R.
; APPLICANT: CARTER, P.J.
; APPLICANT: MERCHANT, A.M.
; APPLICANT: PRESTA, L.G.
; TITLE OF INVENTION: METHOD FOR MAKING MULTISPECIFIC ANTIBODIES HAVING
; TITLE OF INVENTION: HETEROMULTIMERIC AND COMMON COMPONENTS
; FILE REFERENCE: P1099C1 a
; CURRENT APPLICATION NUMBER: US/09/373,403
; CURRENT FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: US 08/850,058
; PRIOR FILING DATE: 1997-05-02
; NUMBER OF SEQ ID NOS: 26
; SEQ ID NO 18
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Recombinant
US-09-373-403-18

Query Match 19.3%; Score 21; DB 11; Length 50;
Best Local Similarity 100.0%; Pred. No. 7.6e-13;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 72 TASLTISGLQAEDEADYYCSS 92
||||||||||||||||||||||
Db 12 TASLTISGLQAEDEADYYCSS 32

RESULT 23
US-09-373-403-19
; Sequence 19, Application US/09373403
; Publication No. US20030207346A1
; GENERAL INFORMATION:
; APPLICANT: ARATHOON, W. R.
; APPLICANT: CARTER, P.J.
; APPLICANT: MERCHANT, A.M.
; APPLICANT: PRESTA, L.G.
; TITLE OF INVENTION: METHOD FOR MAKING MULTISPECIFIC ANTIBODIES HAVING
; TITLE OF INVENTION: HETEROMULTIMERIC AND COMMON COMPONENTS
; FILE REFERENCE: P1099C1 a
; CURRENT APPLICATION NUMBER: US/09/373,403
; CURRENT FILING DATE: 1999-08-12

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;  PRIOR APPLICATION NUMBER: US 08/850,058
;  PRIOR FILING DATE: 1997-05-02
;  NUMBER OF SEQ ID NOS: 26
; SEQ ID NO 19
;    LENGTH: 50
;    TYPE: PRT
;    ORGANISM: Artificial sequence
;    -FEATURE:
;    OTHER INFORMATION: Recombinant
US-09-373-403-19

  Query Match             19.3%;  Score 21;  DB 11;  Length 50;
  Best Local Similarity   100.0%;  Pred. No. 7.6e-13;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         72 TASLTISGLQAEDEADYYCSS 92
              |||||||||||||||||||||
Db         12 TASLTISGLQAEDEADYYCSS 32


RESULT 24
US-09-373-403-20
; Sequence 20, Application US/09373403
; Publication No. US20030207346A1
; GENERAL INFORMATION:
;  APPLICANT: ARATHOON, W. R.
;  APPLICANT:  CARTER, P.J.
;  APPLICANT:  MERCHANT, A.M.
;  APPLICANT:  PRESTA, L.G.
;  TITLE OF INVENTION: METHOD FOR MAKING MULTISPECIFIC ANTIBODIES HAVING
;  TITLE OF INVENTION:  HETEROMULTIMERIC AND COMMON COMPONENTS
;  FILE REFERENCE: P1099C1 a
;  CURRENT APPLICATION NUMBER: US/09/373,403
;  CURRENT FILING DATE:  1999-08-12
;  PRIOR APPLICATION NUMBER: US 08/850,058
;  PRIOR FILING DATE: 1997-05-02
;  NUMBER OF SEQ ID NOS: 26
; SEQ ID NO 20
;    LENGTH: 50
;    TYPE: PRT
;    ORGANISM: Artificial sequence
;    FEATURE:
;    OTHER INFORMATION: Recombinant
;    NAME/KEY: Unsure
;    LOCATION: 9
;    OTHER INFORMATION: Unknown amino acid
US-09-373-403-20

  Query Match             19.3%;  Score 21;  DB 11;  Length 50;
  Best Local Similarity   100.0%;  Pred. No. 7.6e-13;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         72 TASLTISGLQARDEADYYCSS 92
              |||||||||||||||||||||
Db         12 TASLTISGLQAEDEADYYCSS 32


RESULT 25
US-09-373-403-21
; Sequence 21, Application US/09373403
; Publication No. US20030207346A1
; GENERAL INFORMATION:
;  APPLICANT: ARATHOON, W. R.
;  APPLICANT:  CARTER, P.J.
;  APPLICANT:  MERCHANT, A.M.
;  APPLICANT:  PRESTA, L.G.
;  TITLE OF INVENTION: METHOD FOR MAKING MULTISPECIFIC ANTIBODIES HAVING
;  TITLE OF INVENTION:  HETEROMULTIMERIC AND COMMON COMPONENTS
;  FILE REFERENCE: P1099C1 a
;  CURRENT APPLICATION NUMBER: US/09/373,403
;  CURRENT FILING DATE:  1999-08-12
;  PRIOR APPLICATION NUMBER: US 08/850,058
;  PRIOR FILING DATE: 1997-05-02
;  NUMBER OF SEQ ID NOS: 26
; SEQ ID NO 21
;    LENGTH: 50
;    TYPE: PRT
;    ORGANISM: Artificial sequence
;    FEATURE:
;    OTHER INFORMATION: Recombinant
US-09-373-403-21

  Query Match             19.3%;  Score 21;  DB 11;  Length 50;
  Best Local Similarity   100.0%;  Pred. No. 7.6e-13;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         72 TASLTISGLQAEDEADYYCSS 92
              |||||||||||||||||||||
Db         12 TASLTISGLQAEDEADYYCSS 32


Search completed: March 15, 2004, 07:45:17
Job time : 35 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: March 15, 2004, 07:39:39 ; Search time 38 Seconds
(without alignments)
905.039 Million cell updates/sec

Title: US-09-620-955B-4
Perfect score: 109
Sequence: 1 QSALTQPASVSGSPGQSITI.....CSSFANSGPLFGGGTKVTVL 109

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1017041 seqs, 315518202 residues

Word size : 0

Total number of hits satisfying chosen parameters: 199917

Minimum DB seq length: 0
Maximum DB seq length: 109

Post-processing: Listing first 100 summaries

Database : SPTREMBL_25:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	11	10.1	17	4	Q9UC72	Q9uc72 homo sapien
2	10	9.2	81	4	Q7Z2E8	Q7z2e8 homo sapien
3	10	9.2	107	4	Q9UL81	Q9ul81 homo sapien
4	10	9.2	107	4	Q96SA9	Q96sa9 homo sapien
5	10	9.2	107	4	Q9NSD6	Q9nsd6 homo sapien
6	8	7.3	93	4	Q9UL76	Q9ul76 homo sapien
7	8	7.3	101	4	Q8IZD8	Q8izd8 homo sapien
8	8	7.3	107	4	Q9UL82	Q9ul82 homo sapien
9	8	7.3	108	4	Q96SB0	Q96sb0 homo sapien
10	7	6.4	109	4	Q9UL85	Q9ul85 homo sapien
11	7	6.4	109	4	Q9UL78	Q9ul78 homo sapien
12	6	5.5	24	5	Q9TWK4	Q9twk4 mytilus edu
13	6	5.5	53	5	Q967G7	Q967g7 leishmania
14	6	5.5	57	10	Q7X1V6	Q7x1v6 oryza sativ
15	6	5.5	57	16	Q9PNW1	Q9pnw1 campylobact
16	6	5.5	60	10	Q7Y024	Q7y024 oryza sativ
17	6	5.5	61	16	Q53965	Q53965 streptomyce
18	6	5.5	63	4	Q9I4Z8	Q9i4z8 pseudomonas
19	6	5.5	63	16	Q7V7R8	Q7v7r8 prochloroco
20	6	5.5	68	16	Q7UWW3	Q7uww3 rhodopirell
21	6	5.5	69	4	Q9I4H8	Q9i4h8 pseudomonas
22	6	5.5	69	16	Q8XBP2	Q8xbp2 escherichia
23	6	5.5	69	16	Q88MP8	Q88mp8 pseudomonas
24	6	5.5	71	16	Q89E16	Q89e16 bradyrhizob
25	6	5.5	71	16	Q82Z39	Q82z39 enterococcu
26	6	5.5	72	5	Q9GP92	Q9gp92 caenorhabdi
27	6	5.5	73	16	Q87Y28	Q87y28 pseudomonas
28	6	5.5	76	16	Q837I2	Q837i2 enterococcu
29	6	5.5	80	2	Q7X1B4	Q7x1b4 leptospiril
30	6	5.5	87	12	Q69540	Q69540 human herpe
31	6	5.5	87	12	Q69538	Q69538 human herpe
32	6	5.5	90	4	Q14778	Q14778 homo sapien
33	6	5.5	91	16	Q88NJ8	Q88nj8 pseudomonas
34	6	5.5	95	2	Q7X105	Q7x105 xanthomonas
35	6	5.5	97	11	Q9JL76	Q9jl76 mus musculu
36	6	5.5	99	10	Q9NZ47	Q9nz47 arabidopsis
37	6	5.5	99	11	Q9JL74	Q9jl74 mus musculu
38	6	5.5	100	6	O77624	O77624 bos taurus
39	6	5.5	101	11	Q9JL78	Q9jl78 mus musculu
40	6	5.5	103	11	Q9JL80	Q9jl80 mus musculu
41	6	5.5	103	12	Q91LH1	Q91lh1 white spot
42	6	5.5	103	16	Q92Z25	Q92z25 rhizobium m
43	6	5.5	104	11	Q9JL82	Q9jl82 mus musculu
44	6	5.5	105	4	Q8WVJ6	Q8wvj6 homo sapien
45	6	5.5	105	16	Q8XF37	Q8xf37 salmonella
46	6	5.5	106	11	Q9JL84	Q9jl84 mus musculu
47	6	5.5	107	15	Q7ZC22	Q7zc22 human immun
48	6	5.5	108	11	Q8VIJ0	Q8vij0 mus musculu
49	6	5.5	109	6	Q9NUW5	Q9nuw5 oryctolagus
50	6	5.5	109	11	Q920B6	Q920e6 mus musculu
51	6	5.5	109	11	Q9ET13	Q9et13 mus musculu
52	5	4.6	14	4	Q7Z7E2	Q7z7e2 homo sapien
53	5	4.6	15	10	Q9S924	Q9s924 brassica ol
54	5	4.6	17	10	Q9S8E7	Q9s8e7 brassica ol
55	5	4.6	18	10	Q9S8L5	Q9s8l5 zea mays (m
56	5	4.6	19	10	Q9S921	Q9s921 brassica ol
57	5	4.6	20	5	Q26805	Q26805 trypanosoma
58	5	4.6	20	5	Q27385	Q27385 trypanosoma
59	5	4.6	20	6	Q9TR56	Q9tr56 sus scrofa
60	5	4.6	23	10	Q7Y0B6	Q7y0b6 oryza sativ
61	5	4.6	24	5	Q8WT34	Q8wt34 leishmania
62	5	4.6	25	4	Q9UCQ0	Q9ucq0 homo sapien
63	5	4.6	26	2	Q9R5K6	Q9r5k6 campylobact
64	5	4.6	26	12	Q9QRV0	Q9qrv0 hepatitis c
65	5	4.6	26	12	Q9QRU9	Q9qru9 hepatitis c
66	5	4.6	28	2	Q05574	Q05574 prochloroth
67	5	4.6	29	2	Q938P6	Q938p6 borrelia bu
68	5	4.6	30	4	Q9HBG2	Q9hbg2 homo sapien
69	5	4.6	30	11	P97627	P97627 rattus norv
70	5	4.6	32	2	Q45534	Q45534 bacillus su
71	5	4.6	32	3	P78614	P78614 emericella
72	5	4.6	33	12	Q83672	Q83672 measles vir
73	5	4.6	34	16	Q8F7E7	Q8f7e7 leptospira
74	5	4.6	34	16	Q8CTU8	Q8ctu8 staphylococ
75	5	4.6	35	2	Q45807	Q45807 clostridium
76	5	4.6	35	13	Q9PRP0	Q9prp0 gallus gall
77	5	4.6	35	15	Q7SLE9	Q7sle9 human immun
78	5	4.6	36	10	Q9SAQ4	Q9saq4 oryza sativ
79	5	4.6	37	16	Q8F4B5	Q8f4b5 leptospira
80	5	4.6	38	16	Q6XE41	Q6xe41 chlorobium
81	5	4.6	38	16	Q7UUM5	Q7uum5 rhodopirell
82	5	4.6	39	16	Q8UEV3	Q8uev3 agrobacteri
83	5	4.6	41	2	Q7X110	Q7x110 leptospiril
84	5	4.6	41	5	P91022	P91022 caenorhabdi
85	5	4.6	41	6	Q9TSB4	Q9tsb4 bos taurus
86	5	4.6	41	16	Q8F6K7	Q8f6k7 leptospira
87	5	4.6	41	16	Q8EJM7	Q8ejm7 shewanella
88	5	4.6	41	16	Q87Z63	Q87z63 pseudomonas
89	5	4.6	41	16	Q7VND1	Q7vnd1 haemophilus

90	5	4.6	42	16	Q81MR8	Q81mr8 bacillus an
91	5	4.6	42	16	Q81YL0	Q81yl0 bacillus ce
92	5	4.6	43	16	Q8RV57	Q8rv57 staphylococ
93	5	4.6	44	3	Q8J1F0	Q8j1f0 fusarium sp
94	5	4.6	45	4	Q9UDH0	Q9udh0 homo sapien
95	5	4.6	45	4	Q8NEA2	Q8nea2 homo sapien
96	5	4.6	45	6	O97730	O97730 cabassous u
97	5	4.6	46	2	Q9EUR0	Q9eur0 streptococc
98	5	4.6	46	2	Q9S604	Q9s604 escherichia
99	5	4.6	46	2	Q9F1F0	Q9f1f0 enterococcu
100	5	4.6	46	2	Q7WXJ6	Q7wxj6 alcaligenes

ALIGNMENTS

```
RESULT 1
Q9UC72
ID   Q9UC72       PRELIMINARY;      PRT;   17 AA.
AC   Q9UC72;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Amyloid L (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=95340562; PubMed=7615568;
RA   Castano E.M., Prelli F., Pras M., Frangione B.;
RT   "Apolipoprotein E carboxyl-terminal fragments are complexed to
RT   amyloids A and L. Implications for amyloidogenesis and Alzheimer's
RT   disease.";
RL   J. Biol. Chem. 270:17610-17615(1995).
SQ   SEQUENCE   17 AA;  1628 MW;  E3FBB99833638249 CRC64;

  Query Match          10.1%;  Score 11;  DB 4;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 0.00032;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 SALTQPASVSG 12
              ||||||||||| |
Db          1 SALTQPASVSG 11


RESULT 2
Q7Z2E8
ID   Q7Z2E8       PRELIMINARY;      PRT;   81 AA.
AC   Q7Z2E8;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Rearranged Vl3l segment (Rearranged Vl3l gene segment)
DE   (Fragment).
GN   VL3L.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Hodgkin lymphoma, and Mantle cell lymphoma;
RA   Tinguely M., Rosenquist R., Sundstroem C., Amini R.M., Kuppers R.,
RA   Hansmann M.L., Brauninger A.;
RT   "Analysis of a clonally related mantle cell and Hodgkin lymphoma
RT   indicates Epstein-Barr virus infection of a Hodgkin/Reed-Sternberg
RT   cell precursor in a germinal center.";
RL   Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ564423; CAD92030.1; -.
DR   EMBL; AJ564424; CAD92031.1; -.
FT   NON_TER      1      1
FT   NON_TER      81     81
SQ   SEQUENCE   81 AA;  8702 MW;  CFF1D4666B794C9F CRC64;

  Query Match          9.2%;  Score 10;  DB 4;  Length 81;
  Best Local Similarity   100.0%;  Pred. No. 0.015;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          81 QAEDEADYYC 90
               ||||||||||
Db          59 QAEDEADYYC 68


RESULT 3
Q9UL81
ID   Q9UL81       PRELIMINARY;      PRT;   107 AA.
AC   Q9UL81;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Myosin-reactive immunoglobulin light chain variable region
DE   (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF035033; AAD56269.1; -.
DR   HSSP; P01607; 1REI.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_V.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGV; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER      1      1
FT   NON_TER    107    107
SQ   SEQUENCE   107 AA;  11501 MW;  070549FDE0754748 CRC64;

  Query Match          9.2%;  Score 10;  DB 4;  Length 107;
  Best Local Similarity   100.0%;  Pred. No. 0.019;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          75 LTISGLQAED 84
               ||||||||||
Db          73 LTISGLQAED 82


RESULT 4
Q96SA9
ID   Q96SA9       PRELIMINARY;      PRT;   107 AA.
AC   Q96SA9;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Anti-streptococcal/anti-myosin immunoglobulin kappa light chain
DE   variable region (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98375893; PubMed=9712075;
RA   Adderson E.E., Shikhman A.R., Ward K.E., Cunningham M.W.;
RT   "Molecular analysis of polyreactive monoclonal antibodies from
RT   rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin
RT   antibody V region genes.";
```

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RL   J. Immunol. 161:2020-2031(1998).
DR   EMBL; U96396; AAB68785.1; -.
DR   PIR; B49047; B49047.
DR   PIR; S34083; S34083.
DR   PIR; S34086; S34086.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER      1      1
FT   NON_TER    107    107
SQ   SEQUENCE   107 AA;  11520 MW;  4BB43E9CSB577F16 CRC64;

  Query Match             9.2%;  Score 10;  DB 4;  Length 107;
  Best Local Similarity   100.0%;  Pred. No. 0.019;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          42 PGKAPKLLIY 51
               ||||||||||
Db          40 PGKAPKLLIY 49


RESULT 5
Q9NSD6
ID   Q9NSD6       PRELIMINARY;      PRT;   107 AA.
AC   Q9NSD6;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lymphocytes;
RA   Hohmann A.;
RT   "Autoimmunity.";
RL   Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; L43092; AAA69746.2; -.
DR   HSSP; P01709; 2MCG.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER      1      1
FT   NON_TER    107    107
SQ   SEQUENCE   107 AA;  11306 MW;  A2B04B37187A5F00 CRC64;

  Query Match             9.2%;  Score 10;  DB 4;  Length 107;
  Best Local Similarity   100.0%;  Pred. No. 0.019;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          81 QAEDEADYYC 90
               ||||||||||
Db          76 QAEDEADYYC 85


RESULT 6
Q9UL76
ID   Q9UL76       PRELIMINARY;      PRT;    93 AA.
AC   Q9UL76;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Myosin-reactive immunoglobulin light chain variable region
DE   (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF035038; AAD56274.1; -.
DR   HSSP; P01709; 2MCG.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER      1      1
FT   NON_TER     93     93
SQ   SEQUENCE   93 AA;  9596 MW;  2F3C1F6FAA6B90AF CRC64;

  Query Match             7.3%;  Score 8;  DB 4;  Length 93;
  Best Local Similarity   100.0%;  Pred. No. 2.3;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          83 EDEADYYC 90
               ||||||||
Db          67 EDEADYYC 74


RESULT 7
Q8IZD8
ID   Q8IZD8       PRELIMINARY;      PRT;   101 AA.
AC   Q8IZD8;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Anti-thyroglobulin light chain variable region (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Jang Y.-J., Chung J., Park J.-Y.;
RT   "Isolation and Sequence Analysis of Monoclonal Anti-Histone and Anti-
RT   Thyroglobulin Single Chain Fv from SLE Patient by Phage Display.";
RL   Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY145644; AAN64328.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00409; IG; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER      1      1
FT   NON_TER    101    101
SQ   SEQUENCE   101 AA;  10374 MW;  1506C2D9AACBA793 CRC64;

  Query Match             7.3%;  Score 8;  DB 4;  Length 101;
  Best Local Similarity   100.0%;  Pred. No. 2.4;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          33 NYVSWYQQ 40
               ||||||||
Db          22 NYVSWYQQ 29


RESULT 8
Q9UL82
ID   Q9UL82       PRELIMINARY;      PRT;   107 AA.
AC   Q9UL82;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
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DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Myosin-reactive immunoglobulin light chain variable region
DE   (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF035032; AAD56268.1; -.
DR   H8SP; P01703; 7FAB.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER      1      1
FT   NON_TER    107    107
SQ   SEQUENCE   107 AA;  11445 MW;  52F0CC1AB26821DC CRC64;

  Query Match             7.3%;  Score 8;  DB 4;  Length 107;
  Best Local Similarity   100.0%;  Pred. No. 2.6;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          83 EDBADYYC 90
               ||||||||
Db          80 EDBADYYC 87



RESULT 9
Q96SB0
ID   Q96SB0       PRELIMINARY;      PRT;   108 AA.
AC   Q96SB0;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Anti-streptococcal/anti-myosin immunoglobulin lambda light chain
DE   variable region (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98375893; PubMed=9712075;
RA   Adderson E.E., Shikhman A.R., Ward K.E., Cunningham M.W.;
RT   "Molecular analysis of polyreactive monoclonal antibodies from
RT   rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin
RT   antibody V region genes.";
RL   J. Immunol. 161:2020-2031(1998).
DR   EMBL; U96394; AAB68783.1; -.
DR   PDB; 1KU4; 29-MAY-02.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER      1      1
SQ   SEQUENCE   108 AA;  11594 MW;  F4B5DC478A043F48 CRC64;

  Query Match             7.3%;  Score 8;  DB 4;  Length 108;
  Best Local Similarity   100.0%;  Pred. No. 2.6;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          63 RFSGSKSG 70
               ||||||||
Db          62 RFSGSKSG 69
                .

RESULT 10
Q9UL85
ID   Q9UL85       PRELIMINARY;      PRT;   109 AA.
AC   Q9UL85;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Myosin-reactive immunoglobulin kappa chain variable region
DE   (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF035029; AAD56265.1; -.
DR   PIR; D30609; D30609.
DR   H8SP; P80362; 1WTL.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER      1      1
FT   NON_TER    109    109
SQ   SEQUENCE   109 AA;  11761 MW;  FB1E43E7C7AFACCC CRC64;

  Query Match             6.4%;  Score 7;  DB 4;  Length 109;
  Best Local Similarity   100.0%;  Pred. No. 30;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          100 FGGGTKV 106
                ||||||
Db           99 FGGGTKV 105



RESULT 11
Q9UL78
ID   Q9UL78       PRELIMINARY;      PRT;   109 AA.
AC   Q9UL78;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Myosin-reactive immunoglobulin light chain variable region
DE   (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF035036; AAD56272.1; -.
DR   PIR; A30601; A30601.
DR   PIR; A30608; A30608.
DR   PIR; B30601; B30601.
DR   PIR; B30607; B30607.
DR   PIR; C30601; C30601.
DR   PIR; C30607; C30607.
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DR   PIR; C30608; C30608.
DR   PIR; D30601; D30601.
DR   PIR; D30607; D30607.
DR   PIR; D30608; D30608.
DR   PIR; F30607; F30607.
DR   PIR; F30608; F30608.
DR   PIR; G30601; G30601.
DR   PIR; G30608; G30608.
DR   PIR; H30607; H30607.
DR   PIR; H30608; H30608.
DR   PIR; I30601; I30601.
DR   PIR; PH0963; PH0963.
DR   PIR; PH0965; PH0965.
DR   PIR; S34096; S34096.
DR   HSSP; P80362; 1WTL.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER     1     1
FT   NON_TER     109   109
SQ   SEQUENCE   109 AA;  11646 MW;  5F675C52EC7EE197 CRC64;

  Query Match             6.4%;  Score 7;  DB 4;  Length 109;
  Best Local Similarity   100.0%;  Pred. No. 30;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         100 FGGGTKV 106
               |||||||
Db          99 FGGGTKV 105


RESULT 12
Q9TWK4
ID   Q9TWK4          PRELIMINARY;      PRT;    24 AA.
AC   Q9TWK4;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Proximal collagen (Fragment).
OS   Mytilus edulis (Blue mussel).
OC   Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorphia; Mytiloida;
OC   Mytiloidea; Mytilidae; Mytilus.
OX   NCBI_TaxID=6550;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=95230211; PubMed=7714453;
RA   Qin W., Waite J.H.;
RT   "Exotic collagen gradients in the byssus of the mussel Mytilus
RT   edulis.";
RL   J. Exp. Biol. 198:633-644(1995).
DR   InterPro; IPR008160; Collagen.
SQ   SEQUENCE   24 AA;  2054 MW;  29A3FB220799A705 CRC64;

  Query Match             5.5%;  Score 6;  DB 5;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 90;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          11 SGSPGG 16
               ||||||
Db           9 SGSPGG 14


RESULT 13
Q967G7
ID   Q967G7          PRELIMINARY;      PRT;    53 AA.
AC   Q967G7;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Putative transporter protein (Fragment).
GN   ACRD.
OS   Leishmania infantum.
OC   Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX   NCBI_TaxID=5671;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=LEM75;
RA   Reguera R.M., Balana-Fouce R., Perez-Pertejo Y., Ordonez-Escudero D.;
RT   "Efflux pumps and drug resistance in Leishmania infantum.";
RL   Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY033147; AAK53064.1; -.
DR   InterPro; IPR001036; Acrflvin_res.
DR   Pfam; PF00873; ACR_tran; 1.
FT   NON_TER     1     1
FT   NON_TER     53    53
SQ   SEQUENCE   53 AA;  5672 MW;  2A78BAB166691BC5 CRC64;

  Query Match             5.5%;  Score 6;  DB 5;  Length 53;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+02;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          67 SKSGDT 72
               ||||||
Db          20 SKSGDT 25


RESULT 14
Q7XIV6
ID   Q7XIV6          PRELIMINARY;      PRT;    57 AA.
AC   Q7XIV6;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein OJ1409_C08.23.
GN   OJ1409_C08.23.
OS   Oryza sativa (japonica cultivar-group).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC   Ehrhartoideae; Oryzeae; Oryza.
OX   NCBI_TaxID=39947;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=cv. Nipponbare;
RA   Sasaki T., Matsumoto T., Yamamoto K.;
RT   "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 7, BAC
RT   clone:OJ1409_C08.";
RL   Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AP003757; BAC79547.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   57 AA;  6041 MW;  D3761E678FA5C1D4 CRC64;

  Query Match             5.5%;  Score 6;  DB 10;  Length 57;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          70 GDTASL 75
               ||||||
Db          36 GDTASL 41


RESULT 15
Q9PXW1
ID   Q9PXW1          PRELIMINARY;      PRT;    57 AA.
AC   Q9PXW1;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Putative lipoprotein.
GN   CJ0978C.
OS   Campylobacter jejuni.
OC   Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
OC   Campylobacteraceae; Campylobacter.
OX   NCBI_TaxID=197;
RN   [1]
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RP   SEQUENCE FROM N.A.
RC   STRAIN=NCTC 11168;
RX   MEDLINE=20150912; PubMed=10688204;
RA   Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,
RA   Basham D., Chillingworth T., Davies R.M., Feltwell T., Holroyd S.,
RA   Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
RA   Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,
RA   Whitehead S., Barrell B.G.,
RT   "The genome sequence of the food-borne pathogen Campylobacter jejuni
RT   reveals hypervariable sequences.";
RL   Nature 403:665-668(2000).
DR   EMBL; AL139076; CAB73234.1; -.
DR   PIR; G81372; G81372.
DR   InterPro; IPR000437; Prok_lipoprot_S.
DR   PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
KW   Complete proteome.
SQ   SEQUENCE   57 AA;  6645 MW;  3C614BC78F77C5B9 CRC64;

  Query Match           5.5%;  Score 6;  DB 16;  Length 57;
  Best Local Similarity  100.0%;  Pred. No. 2e+02;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          59 GISNRF 64
               ||||||
Db          23 GISNRF 28


RESULT 16
Q7Y024
ID   Q7Y024       PRELIMINARY;      PRT;    60 AA.
AC   Q7Y024;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein OJ1112_G08.18.
GN   OJ1112_G08.18.
OS   Oryza sativa (japonica cultivar-group).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC   Ehrhartoideae; Oryzeae; Oryza.
OX   NCBI_TaxID=39947;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=cv. Nipponbare;
RA   Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Jones K.M.,
RA   Overton II L.L., Tsitrin T., Kim M.M., Bera J.J., Jin S.S.,
RA   Fadrosh D.W., Tallon L.J., Koo H., Zismann V., Hsiao J., Blunt S.,
RA   Vanaken S.S., Riedmuller S.B., Utterback T.T., Feldblyum T.V.,
RA   Yang Q.Q., Haas B.J., Suh B.B., Peterson J.J., Quackenbush J.,
RA   White O., Salzberg S.L., Fraser C.M.,
RT   "Oryza sativa chromosome 3 BAC OJ1112_G08 genomic sequence.";
RL   Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=cv. Nipponbare;
RA   Buell R.;
RL   Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AC135225; AAP68359.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   60 AA;  6991 MW;  48C4E1775DE8F4FA CRC64;

  Query Match           5.5%;  Score 6;  DB 10;  Length 60;
  Best Local Similarity  100.0%;  Pred. No. 2e+02;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          91 SSFANS 96
               ||||||
Db          33 SSFANS 38


RESULT 17
Q53965
ID   Q53965       PRELIMINARY;      PRT;    61 AA.
AC   Q53965;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   EXCISIONASE.
GN   XIS OR SCO4616 OR SCD39.16C.
OS   Streptomyces coelicolor.
OG   Plasmid pRI1724.
OC   Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC   Streptomycineae; Streptomycetaceae; Streptomyces.
OX   NCBI_TaxID=1902;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   PLASMID=pRI1724;
RX   MEDLINE=93255953; PubMed=8387993;
RA   Brasch M.A., Pettis G.S., Lee S.C., Cohen S.N.;
RT   "Localization and nucleotide sequences of genes mediating site-
RT   specific recombination of the SLP1 element in Streptomyces lividans.";
RL   J. Bacteriol. 175:3067-3074(1993).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=A3(2);
RA   Brown S.P., Harris D.;
RL   Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=A3(2);
RA   Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.;
RL   Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=A3(2);
RX   MEDLINE=97000351; PubMed=8843436;
RA   Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J.,
RA   Kinashi H., Hopwood D.A.;
RT   "A set of ordered cosmids and a detailed genetic and physical map for
RT   the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
RL   Mol. Microbiol. 21:77-96(1996).
RN   [5]
RP   SEQUENCE FROM N.A.
RC   STRAIN=A3(2) / M145;
RX   MEDLINE=21996410; PubMed=12000953;
RA   Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA   Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA   Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA   Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA   Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
RA   Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
RA   Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA   Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
RA   Hopwood D.A.,
RT   "Complete genome sequence of the model actinomycete Streptomyces
RT   coelicolor A3(2).";
RL   Nature 417:141-147(2002).
DR   EMBL; X71358; CAA50493.1; -.
DR   EMBL; AL939120; CAC08269.1; -.
DR   GO; GO:0046821; C:extrachromosomal DNA; IEA.
KW   Plasmid; Complete proteome.
SQ   SEQUENCE   61 AA;  7103 MW;  CCC67B2F0D173512 CRC64;

  Query Match           5.5%;  Score 6;  DB 16;  Length 61;
  Best Local Similarity  100.0%;  Pred. No. 2.1e+02;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          43 GKAPKL 48
               ||||||
Db          30 GKAPKL 35


RESULT 18
Q9I4Z8
ID   Q9I4Z8       PRELIMINARY;      PRT;    63 AA.
AC   Q9I4Z8;
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DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Probable cold-shock protein.
GN   PA0961.
OS   Pseudomonas aeruginosa.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC   Pseudomonadaceae; Pseudomonas.
OX   NCBI_TaxID=287;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ATCC 15692 / PAO1;
RX   MEDLINE=20437337; PubMed=10984043;
RA   Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
RA   Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA   Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
RA   Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA   Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA   Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT   "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
RT   opportunistic pathogen.";
RL   Nature 406:959-964(2000).
CC   -!- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE COLD-SHOCK DOMAIN (CSD) FAMILY.
DR   EMBL; AE004530; AAG04350.1; -.
DR   PIR; C83524; C83524.
DR   HSSP; P41016; 1CSO.
DR   GO; GO:0003677; F:DNA binding; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   InterPro; IPR000059; Cold_shock.
DR   InterPro; IPR008994; Nucleic_acid_OB.
DR   Pfam; PF00313; CSD; 1.
DR   PRINTS; PR00050; COLDSHOCK.
DR   ProDom; PD000621; Cold_shock; 1.
DR   SMART; SM00357; CSP; 1.
DR   PROSITE; PS00352; COLD_SHOCK; 1.
KW   Activator; DNA-binding; Transcription regulation; Complete proteome.
SQ   SEQUENCE   63 AA;  7281 MW;  1219B2AB9C6B6808 CRC64;

  Query Match           5.5%;  Score 6;  DB 16;  Length 63;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          79 GLQAED 84
               ||||||
Db          52 GLQAED 57


RESULT 19
Q7V7R8
ID   Q7V7R8          PRELIMINARY;      PRT;    63 AA.
AC   Q7V7R8;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
GN   PMT0670.
OS   Prochlorococcus marinus (strain MIT 9313).
OC   Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
OC   Prochlorococcus.
OX   NCBI_TaxID=74547;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22825698; PubMed=12917642;
RA   Rocap G., Larimer F.W., Lamerdin J., Malfatti S., Chain P.,
RA   Ahlgren N.A., Arellano A., Coleman M., Hauser L., Hess W.R.,
RA   Johnson Z.I., Land M., Lindell D., Post A.F., Regala W., Shah M.,
RA   Shaw S.L., Steglich C., Sullivan M.B., Ting C.S., Tolonen A.,
RA   Webb E.A., Zinser E.R., Chisholm S.W.;
RT   "Genome divergence in two Prochlorococcus ecotypes reflects oceanic
RT   niche differentiation.";
RL   Nature 424:1042-1047(2003).
DR   EMBL; BX572097; CAE20845.1; -.
KW   Hypothetical protein; Complete proteome.
SQ   SEQUENCE   63 AA;  7090 MW;  E8DCE5102ECE593E CRC64;

  Query Match           5.5%;  Score 6;  DB 16;  Length 63;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          65 SGSKSG 70
               ||||||
Db          26 SGSKSG 31


RESULT 20
Q7UWM3
ID   Q7UWM3          PRELIMINARY;      PRT;    68 AA.
AC   Q7UWM3;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
GN   RB1931.
OS   Rhodopirellula baltica.
OC   Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
OC   Planctomycetaceae; Pirellula.
OX   NCBI_TaxID=117;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=1;
RX   MEDLINE=22735913; PubMed=12853416;
RA   Glockner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,
RA   Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R.,
RA   Schlesner H., Amann R., Reinhardt R.;
RT   "Complete genome sequence of the marine planctomycete Pirellula sp.
RT   strain 1.";
RL   Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303(2003).
DR   EMBL; BX294136; CAD72339.1; -.
KW   Hypothetical protein; Complete proteome.
SQ   SEQUENCE   68 AA;  7494 MW;  7EC1FDF98DB5F67C CRC64;

  Query Match           5.5%;  Score 6;  DB 16;  Length 68;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+02;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          74 SLTISG 79
               ||||||
Db           3 SLTISG 8


RESULT 21
Q9I4H8
ID   Q9I4H8          PRELIMINARY;      PRT;    69 AA.
AC   Q9I4H8;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Probable cold-shock protein.
GN   PA1159.
OS   Pseudomonas aeruginosa.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC   Pseudomonadaceae; Pseudomonas.
OX   NCBI_TaxID=287;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ATCC 15692 / PAO1;
RX   MEDLINE=20437337; PubMed=10984043;
RA   Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
RA   Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA   Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
RA   Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA   Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA   Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT   "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
RT   opportunistic pathogen.";
```

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RL   Nature 406:959-964(2000).
CC   -!- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE COLD-SHOCK DOMAIN (CSD) FAMILY.
DR   EMBL; AE004546; AAG04548.1; -.
DR   PIR; D83500; D83500.
DR   HSSP; P41016; 1CGO.
DR   GO; GO:0003677; F:DNA binding; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   InterPro; IPR002059; Cold_shock.
DR   InterPro; IPR008994; Nucleic_acid_OB.
DR   Pfam; PF00313; CSD; 1.
DR   PRINTS; PR00050; COLDSHOCK.
DR   ProDom; PD000521; Cold_shock; 1.
DR   SMART; SM00357; CSP; 1.
DR   PROSITE; PS00352; COLD_SHOCK; 1.
KW   Activator; DNA-binding; Transcription regulation; Complete proteome.
SQ   SEQUENCE   69 AA;  7725 MW;  00D73040661D64D2 CRC64;

  Query Match             5.5%;  Score 6;  DB 16;  Length 69;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+02;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          79 GLQAED 84
               ||||||
Db          60 GLQAED 65


RESULT 22
Q8XBP2
ID   Q8XBP2       PRELIMINARY;      PRT;    69 AA.
AC   Q8XBP2;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   YbeB protein.
GN   YBEB OR Z0783 OR ECS0675.
OS   Escherichia coli O157:H7.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC   Enterobacteriaceae; Escherichia.
OX   NCBI_TaxID=83334;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=O157:H7 / EDL933 / ATCC 700927;
RX   MEDLINE=21074935; PubMed=11206551;
RA   Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA   Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA   Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA   Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
RA   Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA   Welch R.A., Blattner F.R.;
RT   "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
RL   Nature 409:529-533(2001).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=O157:H7 / RIMD 0509952;
RX   MEDLINE=21156231; PubMed=11258796;
RA   Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA   Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA   Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
RA   Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RT   "Complete genome sequence of enterohemorrhagic Escherichia coli
RT   O157:H7 and genomic comparison with a laboratory strain K-12.";
RL   DNA Res. 8:11-22(2001).
DR   EMBL; AE005242; AAG54971.1; -.
DR   EMBL; AP002552; BAB34098.1; -.
DR   PIR; A24995; QQECP7.
DR   PIR; C90713; C90713.
DR   PIR; G85563; G85563.
DR   InterPro; IPR004394; Iojap.
DR   Pfam; PF02410; DUF143; 1.
DR   TIGRFAMs; TIGR00090; TIGR00090; 1.
KW   Complete proteome.
SQ   SEQUENCE   69 AA;  7678 MW;  A470FC77D9207E12 CRC64;

  Query Match             5.5%;  Score 6;  DB 16;  Length 69;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+02;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          22 CTGTSS 27
               ||||||
Db           4 CTGTSS 9


RESULT 23
Q8SMP8
ID   Q8SMP8       PRELIMINARY;      PRT;    69 AA.
AC   Q8SMP8;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Cold shock protein CspA.
GN   CSPA-1 OR PP1522.
OS   Pseudomonas putida (strain KT2440).
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC   Pseudomonadaceae; Pseudomonas.
OX   NCBI_TaxID=160488;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22423060; PubMed=12534463;
RA   Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
RA   Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
RA   Brinkac L., Beanan M., DeBoy R.T., Daugherty S., Kolonay J.,
RA   Madupu R., Nelson W., White O., Peterson J., Khouri H., Hance I.,
RA   Chris Lee P., Holtzapple E., Scanlan D., Tran K., Moazzez A.,
RA   Utterback T., Rizzo M., Lee K., Kosack D., Moestl D., Wedler H.,
RA   Lauber J., Stjepandic D., Hoheisel J., Straetz M., Heim S.,
RA   Kiewitz C., Eisen J., Timmis K.N., Duesterhoeft A., Tuemmler B.,
RA   Fraser C.M.;
RT   "Complete genome sequence and comparative analysis of the
RT   metabolically versatile Pseudomonas putida KT2440.";
RL   Environ. Microbiol. 4:799-808(2002).
DR   EMBL; AE016779; AAN67143.1; -.
DR   PIR; PP1522; -.
DR   GO; GO:0003677; F:DNA binding; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   InterPro; IPR002059; Cold_shock.
DR   InterPro; IPR008994; Nucleic_acid_OB.
DR   Pfam; PF00313; CSD; 1.
DR   PRINTS; PR00050; COLDSHOCK.
DR   PROSITE; PS00352; COLD_SHOCK; 1.
KW   Complete proteome.
SQ   SEQUENCE   69 AA;  7673 MW;  5A7E14A10FDA954A CRC64;

  Query Match             5.5%;  Score 6;  DB 16;  Length 69;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+02;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          79 GLQAED 84
               ||||||
Db          60 GLQAED 65


RESULT 24
Q89SI6
ID   Q89SI6       PRELIMINARY;      PRT;    71 AA.
AC   Q89SI6;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Bsr2414 protein.
GN   BSR2414
OS   Bradyrhizobium japonicum.
OC   Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC   Bradyrhizobiaceae; Bradyrhizobium.
OX   NCBI_TaxID=375;
RN   [1]
```

```
RP   SEQUENCE FROM N.A.
RC   STRAIN=USDA 110;
RX   MEDLINE=22484998; PubMed=12597275;
RA   Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
RA   Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
RA   Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
RA   Tabata S.;
RT   "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
RT   Bradyrhizobium japonicum USDA110.";
RL   DNA Res. 9:189-197(2002).
DR   EMBL; AP005943; BAC47679.1; -.
DR   GO; GO:0000155; F:two-component sensor molecule activity; IEA.
DR   GO; GO:0000160; P:two-component signal transduction system (p. . .; IEA.
DR   InterPro; IPR000700; PAS-assoc_C.
DR   PROSITE; PS50113; PAC; 1.
KW   Complete proteome.
SQ   SEQUENCE   71 AA;  7501 MW;  CC91E64E2B507DC5 CRC64;

  Query Match             5.5%;  Score 6;  DB 16;  Length 71;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+02;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         73 ASLTIS 78
              ||||||
Db         61 ASLTIS 66


RESULT 25
Q82Z39
ID   Q82Z39      PRELIMINARY;      PRT;    71 AA.
AC   Q82Z39;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Hypothetical protein.
GN   EF3239.
OS   Enterococcus faecalis (Streptococcus faecalis).
OC   Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX   NCBI_TaxID=1351;
RN   [1] -
RP   SEQUENCE FROM N.A.
RC   STRAIN=V583 / ATCC 700802;
RX   MEDLINE=22550857; PubMed=12663927;
RA   Paulsen I.T., Banerjei L., Myers G.S.A., Nelson K.E., Seshadri R.,
RA   Read T.D., Fouts D.E., Eisen J.A., Gill S.R., Heidelberg J.F.,
RA   Tettelin H., Dodson R.J., Umayam L., Brinkac L., Beanan M.,
RA   Daugherty S., DeBoy R.T., Durkin S., Kolonay J., Madupu R., Nelson W.,
RA   Vamathevan J., Tran B., Upton J., Hansen T., Shetty J., Khouri H.,
RA   Utterback T., Radune D., Ketchum K.A., Dougherty B.A., Fraser C.M.;
RT   "Role of mobile DNA in the evolution of vancomycin-resistant
RT   Enterococcus faecalis.";
RL   Science 299:2071-2074(2003).
DR   EMBL; AE016957; AAO82907.1; -.
DR   TIGR; EF3239; -.
KW   Hypothetical protein; Complete proteome.
SQ   SEQUENCE   71 AA;  7931 MW;  5719F0029D89F7AB CRC64;

  Query Match             5.5%;  Score 6;  DB 16;  Length 71;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+02;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         18 ITISCT 23
              ||||||
Db         40 ITISCT 45


Search completed: March 15, 2004, 07:43:27
Job time : 43 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: March 15, 2004, 07:39:09 ; Search time 17 Seconds
(without alignments)
333.862 Million cell updates/sec

Title: US-09-620-955B-4
Perfect score: 109
Sequence: 1 QSALTQPASVSGSPGQSITI.....CSSPANSGPLPGGGTKVTVL 109

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 141681 seqs, 52070155 residues

Word size : 0

Total number of hits satisfying chosen parameters: 17605

Minimum DB seq length: 0
Maximum DB seq length: 109

Post-processing: Listing first 100 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	19	17.4	109	1	LV2S_HUMAN	P01708 homo sapien
2	12	11.0	103	1	LV1S_HUMAN	P01703 homo sapien
3	11	10.1	108	1	KV1B_HUMAN	P01594 homo sapien
4	11	10.1	108	1	KV1P_HUMAN	P01608 homo sapien
5	10	9.2	107	1	LV4C_HUMAN	P01717 homo sapien
6	10	9.2	108	1	KV1K_HUMAN	P01603 homo sapien
7	10	9.2	108	1	KV1O_HUMAN	P01607 homo sapien
8	10	9.2	108	1	KV5Q_MOUSE	P01650 mus musculu
9	10	9.2	108	1	KV5R_MOUSE	P01651 mus musculu
10	10	9.2	108	1	KV5S_MOUSE	P01652 mus musculu
11	10	9.2	108	1	KV5T_MOUSE	P01653 mus musculu
12	10	9.2	108	1	LV3A_HUMAN	P01714 homo sapien
13	9	8.3	108	1	KV1C_HUMAN	P01611 homo sapien
14	9	8.3	109	1	KV1T_HUMAN	P01612 homo sapien
15	8	7.3	108	1	KV1F_HUMAN	P01592 homo sapien
16	8	7.3	108	1	KV1L_HUMAN	P01604 homo sapien
17	8	7.3	109	1	LV1F_HUMAN	P04208 homo sapien
18	8	7.3	109	1	LV1I_HUMAN	P06888 homo sapien
19	7	6.4	94	1	KV1R_RABIT	P01692 oryctolagus
20	7	6.4	106	1	LV4A_HUMAN	P01715 homo sapien
21	7	6.4	106	1	LV4B_HUMAN	P01716 homo sapien
22	7	6.4	106	1	LV4E_HUMAN	P06889 homo sapien
23	7	6.4	108	1	KV1M_HUMAN	P01605 homo sapien
24	7	6.4	108	1	KV1Y_HUMAN	P80362 homo sapien
25	7	6.4	108	1	LV5A_HUMAN	P01719 homo sapien
26	6	5.5	81	1	EX7S_PSESM	Q889p9 pseudomonas
27	6	5.5	91	1	CS54_THINE	P25938 thiobacillu
28	6	5.5	98	1	V5PA_CERCE	P81038 cerastes ce
29	6	5.5	102	1	YBEB_HAEIN	P44471 haemophilus
30	6	5.5	105	1	YBEB_ECOLI	P05848 escherichia
31	6	5.5	106	1	LV4D_HUMAN	P01718 homo sapien
32	6	5.5	107	1	KV1D_HUMAN	P01596 homo sapien
33	6	5.5	107	1	KV6A_MOUSE	P01675 mus musculu
34	6	5.5	107	1	KV6D_MOUSE	P01678 mus musculu
35	6	5.5	108	1	KV05_RABIT	P01686 oryctolagus
36	6	5.5	108	1	KV06_RABIT	P01687 oryctolagus
37	6	5.5	108	1	KV07_RABIT	P01688 oryctolagus
38	6	5.5	108	1	KV08_RABIT	P01689 oryctolagus
39	6	5.5	108	1	KV1A_HUMAN	P01593 homo sapien
40	6	5.5	108	1	KV1C_HUMAN	P01595 homo sapien
41	6	5.5	108	1	KV1E_HUMAN	P01597 homo sapien
42	6	5.5	108	1	KV1G_HUMAN	P01599 homo sapien
43	6	5.5	108	1	KV1V_HUMAN	P04430 homo sapien
44	6	5.5	108	1	KV5J_MOUSE	P01643 mus musculu
45	6	5.5	108	1	KV5K_MOUSE	P01644 mus musculu
46	6	5.5	108	1	KV5L_MOUSE	P01645 mus musculu
47	6	5.5	108	1	KV5M_MOUSE	P01646 mus musculu
48	6	5.5	108	1	KV5N_MOUSE	P01647 mus musculu
49	6	5.5	108	1	KV5O_MOUSE	P01648 mus musculu
50	6	5.5	108	1	KV5P_MOUSE	P01649 mus musculu
51	6	5.5	108	1	KV5U_MOUSE	P04946 mus musculu
52	6	5.5	109	1	KV14_RABIT	P01695 oryctolagus
53	6	5.5	109	1	KV4D_HUMAN	P83593 homo sapien
54	5	4.6	12	1	HCY1_CARMA	P83176 carcinus ma
55	5	4.6	27	1	LIPS_BOVIN	P16386 bos taurus
56	5	4.6	35	1	SCXR_PANIM	P55928 pandinus im
57	5	4.6	47	1	FLGD_YEREN	Q56895 yersinia en
58	5	4.6	47	1	SCXA_PANIM	P55927 pandinus im
59	5	4.6	51	1	INE1_HUMAN	O15229 homo sapien
60	5	4.6	54	1	YNAL_ECOLI	P42625 escherichia
61	5	4.6	57	1	YQGO_BACSU	P54492 bacillus su
62	5	4.6	58	1	Y293_TREPA	O83316 treponema p
63	5	4.6	59	1	SSH1_BACAA	Q81V87 bacillus an
64	5	4.6	59	1	SSH1_BACCR	Q81L11 bacillus ce
65	5	4.6	62	1	RL28_STRPN	Q97ae1 streptococc
66	5	4.6	63	1	CE3S_HYPCU	P50721 hyphantria
67	5	4.6	64	1	PPIF_BOVIN	P30404 bos taurus
68	5	4.6	66	1	R24S_HALMA	P14116 haloarcula
69	5	4.6	75	1	RL31_CHLTE	Q8Ke50 chlorobium
70	5	4.6	77	1	RAC1_CAVPO	P80236 cavia porce
71	5	4.6	77	1	SECG_CORGL	Q9x469 corynebacte
72	5	4.6	77	1	SECG_MYCLE	P38388 mycobacteri
73	5	4.6	77	1	SECG_MYCTU	O06819 mycobacteri
74	5	4.6	78	1	DSVD_DESVH	Q46582 desulfovibr
75	5	4.6	78	1	RPOH_METAC	Q8tJ68 methanosarc
76	5	4.6	78	1	RPOH_METMA	Q8puq8 methanosarc
77	5	4.6	78	1	RPOH_METVA	P41559 methanococc
78	5	4.6	80	1	CD24_HUMAN	P25063 homo sapien
79	5	4.6	85	1	HKL6_MAIZE	P56664 zea mays (m
80	5	4.6	85	1	HKL7_MAIZE	P56665 zea mays (m
81	5	4.6	88	1	HKL2_MAIZE	P56660 zea mays (m
82	5	4.6	88	1	RL34_METTH	O26137 methanobact
83	5	4.6	90	1	CH10_BORBU	O51683 borrelia bu
84	5	4.6	90	1	PSBH_PROHO	P31095 prochloroth
85	5	4.6	90	1	RS16_BACHD	Q9ka11 bacillus ha
86	5	4.6	92	1	KV09_RABIT	P01690 oryctolagus
87	5	4.6	92	1	RS19_BORBU	P94371 borrelia bu
88	5	4.6	92	1	YH75_PASMU	Q9ck59 pasteurella
89	5	4.6	93	1	YQ32_MYCTU	P71931 mycobacteri
90	5	4.6	95	1	HMGY_MOUSE	P17095 mus musculu
91	5	4.6	95	1	SECE_STRGR	P36690 streptomyce
92	5	4.6	96	1	V129_POWPV	P15911 fowlpox vir
93	5	4.6	97	1	NLPD_YEREN	P47764 yersinia en
94	5	4.6	98	1	ACYM_HORSE	P00818 equus cabal
95	5	4.6	99	1	CH10_ORYLA	Q9w6x3 oryzias lat
96	5	4.6	99	1	YGAV_ECOLI	P77295 escherichia
97	5	4.6	100	1	DBF6_HUMAN	Q01524 homo sapien
98	5	4.6	100	1	KV3C_HUMAN	P01621 homo sapien
99	5	4.6	101	1	CH10_HUMAN	O04984 homo sapien
100	5	4.6	101	1	CH10_MOUSE	Q64433 mus musculu

ALIGNMENTS

RESULT 1

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LV2E_HUMAN
ID   LV2E_HUMAN      STANDARD;       PRT;   109 AA.
AC   P01706;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Ig lambda chain V-II region BUR.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=80006606; PubMed=113407;
RA   Infante A.J., Putnam F.W.;
RT   "Primary structure of a human IgA1 immunoglobulin. V. Amino acid
RT   sequence of a human IgA lambda light chain.";
RL   J. Biol. Chem. 254:9006-9016(1979).
CC   -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE KERN+ AND MCG+
CC       MARKERS.
CC   -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR   PIR; A01974; L2HUBR.
DR   HSSP; P01709; 2MCG.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_V.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Pyrrolidone carboxylic acid.
FT   DOMAIN      1      106      IG-LIKE.
FT   MOD_RES     1        1      PYRROLIDONE CARBOXYLIC ACID.
FT   DISULFID    22      90      BY SIMILARITY.
FT   SITE        91      91      APPEARS TO BE A FREE BUT UNREACTIVE
FT                               SULPHYDRYL GROUP.
FT   NON_TER    109     109
SQ   SEQUENCE   109 AA;  11506 MW;  BFD8AE1CSD267FAB CRC64;

  Query Match          17.4%;  Score 19;  DB 1;  Length 109;
  Best Local Similarity   100.0%;  Pred. No. 6.6e-13;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          72 TASLTISGLQAEDEADYYC 90
               ||||||||||||||||||| 
Db          72 TASLTISGLQAEDEADYYC 90



RESULT 2
LV1S_HUMAN
ID   LV1S_HUMAN      STANDARD;       PRT;   103 AA.
AC   P01703;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Ig lambda chain V-I region NEWM.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=74109253; PubMed=4814727;
RA   Chen B.L., Poljak R.J.;
RT   "Amino acid sequence of the (lambda) light chain of a human myeloma
RT   immunoglobulin (IgG New).";
RL   Biochemistry 13:1295-1302(1974).
RN   [2]
RP   X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX   MEDLINE=78066916; PubMed=618887;
RA   Saul F.A., Amzel L.M., Poljak R.J.;
RT   "Preliminary refinement and structural analysis of the Fab fragment
RT   from human immunoglobulin new at 2.0-A resolution.";
RL   J. Biol. Chem. 253:585-597(1978).
CC   -!- MISCELLANEOUS: THE STRUCTURE OF THE FAB FRAGMENT OF THE IGG1
CC       MYELOMA PROTEIN NEWM WAS DETERMINED.
CC   -!- MISCELLANEOUS: THE ABSENCE OF SEVEN RESIDUES FOUND IN OTHER LAMBDA
CC       CHAINS WAS CONFIRMED BY X-RAY CRYSTALLOGRAPHIC ANALYSIS.
CC   -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE G2+ MARKER.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR   PIR; A01968; L1HUNM.
DR   PDB; 7FAB; 11-JAN-94.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_V.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; 3D-structure; Pyrrolidone carboxylic acid.
FT   DOMAIN      1      99      IG-LIKE.
FT   MOD_RES     1       1      PYRROLIDONE CARBOXYLIC ACID.
FT   STRAND      4       5
FT   STRAND      9      12
FT   TURN       14      15
FT   STRAND     18      23
FT   TURN       26      28
FT   HELIX      29      31
FT   TURN       32      32
FT   STRAND     36      40
FT   TURN       42      43
FT   STRAND     47      48
FT   TURN       52      53
FT   STRAND     57      62
FT   TURN       63      64
FT   STRAND     65      70
FT   HELIX      75      77
FT   STRAND     79      87
FT   TURN       88      89
FT   STRAND     90      94
FT   STRAND     97     101
FT   NON_TER   103     103
SQ   SEQUENCE   103 AA;  10904 MW;  32727AD731AE7584 CRC64;

  Query Match          11.0%;  Score 12;  DB 1;  Length 103;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-05;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          79 GLQAEDEADYYC 90
               ||||||||||||
Db          72 GLQAEDEADYYC 83

RESULT 3
KV1B_HUMAN
ID   KV1B_HUMAN      STANDARD;       PRT;   108 AA.
AC   P01594;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Ig kappa chain V-I region AU.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=72189444; PubMed=5028201;
RA   Schiechl H., Hilschmann N.;
RT   "Rule of antibody structure. The primary structure of a monoclonal
RT   immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones
RT   protein Au).";
RL   Hoppe-Seyler's Z. Physiol. Chem. 353:345-370(1972).
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RN   [2]
RP   X-RAY CRYSTALLOGRAPHY.
RX   MEDLINE=77022433; PubMed=1234024;
RA   Fehlhammer H., Schiffer M., Epp O., Colman P.M., Lattman E.E.,
RA   Schwager P., Steigemann W., Schramm H.J.;
RT   "The structure determination of the variable portion of the
RT   Bence-Jones protein Au.";
RL   Biophys. Struct. Mech. 1:139-146(1975).
CC   -!- MISCELLANEOUS: THE STRUCTURE OF THE V REGION WAS DETERMINED BY
CC       MOLECULAR REPLACEMENT METHODS USING THE KNOWN STRUCTURE OF THE V
CC       REGION OF THE KAPPA CHAIN REI.
CC   -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC   -!- MISCELLANEOUS: This is a Bence-Jones protein.
DR   PIR; A91653; KIHUAU.
DR   PDB; 1JV5; 30-JAN-02.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_V.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Bence-Jones protein; 3D-structure.
FT   DOMAIN       1     23       FRAMEWORK-1.
FT   DOMAIN      24     34       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN      35     49       FRAMEWORK-2.
FT   DOMAIN      50     56       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN      57     88       FRAMEWORK-3.
FT   DOMAIN      89     97       COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN      98    107       FRAMEWORK-4.
FT   DISULFID    23     88       BY SIMILARITY.
FT   NON_TER    108    108
SQ   SEQUENCE   108 AA;  11939 MW;  EB011187EE6F6FB9 CRC64;

  Query Match          10.1%;  Score 11;  DB 1;  Length 108;
  Best Local Similarity   100.0%;  Pred. No. 0.00022;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          42 PGKAPKLLIYD 52
               ||||||||||| |
Db          40 PGKAPKLLIYD 50


RESULT 4
KV1P_HUMAN
ID   KV1P_HUMAN      STANDARD;      PRT;   108 AA.
AC   P01608;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-I region Roy.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=68362076; PubMed=5595110;
RA   Hilschmann N.;
RT   "Chemical structure of 2 kappa-type Bence Jones proteins (Roy and
RT   Cum.).";
RL   Hoppe-Seyler's Z. Physiol. Chem. 348:1077-1080(1967).
RN   [2]
RP   REVISIONS TO 39 AND 41.
RA   Hilschmann N., Barnikol H.U., Hess M., Langer B., Ponstingl H.,
RA   Steinmetz-Kayne M., Suter L., Watanabe S.;
RL   (In) Franek F., Shugar D. (eds.);
RL   Gamma globulins: structure and function, pp.57-74, Academic Press,
RL   New York (1969).
CC   -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
CC       MARKER.
CC   -!- MISCELLANEOUS: This is a Bence-Jones protein.
DR   PIR; A91638; K1HURY.
DR   HSSP; P80362; 1WTL.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_V.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Bence-Jones protein.
FT   DOMAIN       1     23       FRAMEWORK-1.
FT   DOMAIN      24     34       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN      35     49       FRAMEWORK-2.
FT   DOMAIN      50     56       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN      57     88       FRAMEWORK-3.
FT   DOMAIN      89     97       COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN      98    107       FRAMEWORK-4.
FT   DISULFID    23     88       BY SIMILARITY.
FT   NON_TER    108    108
SQ   SEQUENCE   108 AA;  11782 MW;  F5ACED85A313DF3A CRC64;

  Query Match          10.1%;  Score 11;  DB 1;  Length 108;
  Best Local Similarity   100.0%;  Pred. No. 0.00022;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          42 PGKAPKLLIYD 52
               ||||||||||| |
Db          40 PGKAPKLLIYD 50


RESULT 5
LV4C_HUMAN
ID   LV4C_HUMAN      STANDARD;      PRT;   107 AA.
AC   P01717;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Ig lambda chain V-IV region Hil.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=78187276; PubMed=418804;
RA   Lopez de Castro J.A., Chiu Y.-Y.H., Poljak R.J.;
RT   "Amino acid sequence of the variable region of the light (lambda)
RT   chain from human myeloma cryoimmunoglobulin IgG Hil.";
RL   Biochemistry 17:1718-1723(1978).
CC   -!- MISCELLANEOUS: THE SEQUENCE OF THE C REGION IS APPARENTLY
CC       IDENTICAL WITH THAT OF HUMAN SH LAMBDA CHAIN EXCEPT IN HAVING
CC       155-ILE (HIL NUMBERING) INSTEAD OF VAL.
CC   -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR   PIR; A01983; L4HUHL.
DR   HSSP; P80748; 2LOI.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_V.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region.
FT   DOMAIN       1     97       IG-LIKE.
FT   NON_TER    107    107
SQ   SEQUENCE   107 AA;  11517 MW;  A5C8APPE0C0C590A CRC64;

  Query Match          9.2%;  Score 10;  DB 1;  Length 107;
  Best Local Similarity   100.0%;  Pred. No. 0.0025;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy          81 QAEDBADYYC 90
               ||||||||||
Db          78 QAEDBADYYC 87


RESULT 6
KV1K_HUMAN
ID   KV1K_HUMAN      STANDARD;      PRT;   108 AA.
AC   P01603;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-I region Ka.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=76189985; PubMed=818073;
RT   "Comparative structural studies on the light chains of human
RT   immunoglobulins. I. Protein Ka with the Inv(3) allotypic marker.";
RL   J. Biochem. 77:1277-1296(1976).
CC   -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC   -!- MISCELLANEOUS: This is a Bence-Jones protein.
DR   PIR; A01869; K1HUKA.
DR   HSSP; P80362; 1WTL.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_V.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Bence-Jones protein.
FT   DOMAIN          1     23       FRAMEWORK-1.
FT   DOMAIN         24     34       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN         35     49       FRAMEWORK-2.
FT   DOMAIN         50     56       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN         57     88       FRAMEWORK-3.
FT   DOMAIN         89     97       COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN         98    107       FRAMEWORK-4.
FT   DISULFID       23     88       BY SIMILARITY.
FT   NON_TER       108    108
SQ   SEQUENCE   108 AA;  11900 MW;  768839FBED5A2F4B CRC64;

  Query Match             9.2%;  Score 10;  DB 1;  Length 108;
  Best Local Similarity   100.0%;  Pred. No. 0.0025;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          42 PGKAPKLLIY 51
               ||||||||||
Db          40 PGKAPKLLIY 49


RESULT 7
KV1O_HUMAN
ID   KV1O_HUMAN      STANDARD;      PRT;   108 AA.
AC   P01607;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Ig kappa chain V-I region Rei.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=76023758; PubMed=809329;
RA   Palm W., Hilschmann N.;
RT   "The primary structure of a crystalline monoclonal immunoglobulin
RT   kappa-type L-chain, subgroup I (Bence-Jones protein Rei); isolation
RT   and characterization of the tryptic peptides; the complete amino acid
RT   sequence of the protein; a contribution to the elucidation of the
RT   three-dimensional structure of antibodies, in particular their
RT   combining site.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 356:167-191(1975).
RN   [2]
RP   X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX   MEDLINE=76039968; PubMed=1182131;
RA   Epp O., Lattman E.E., Schiffer M., Huber R., Palm W.;
RT   "The molecular structure of a dimer composed of the variable portions
RT   of the Bence-Jones protein REI refined at 2.0-A resolution.";
RL   Biochemistry 14:4943-4952(1975).
CC   -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
CC       MARKER.
CC   -!- MISCELLANEOUS: This is a Bence-Jones protein.
DR   PIR; A91663; K1HURE.
DR   PDB; 1REI; 17-FEB-84.
DR   PDB; 1AR2; 12-NOV-97.
DR   PDB; 1BWW; 29-DEC-99.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_V.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Bence-Jones protein; 3D-structure.
FT   DOMAIN          1     23       FRAMEWORK-1.
FT   DOMAIN         24     34       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN         35     49       FRAMEWORK-2.
FT   DOMAIN         50     56       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN         57     88       FRAMEWORK-3.
FT   DOMAIN         89     97       COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN         98    107       FRAMEWORK-4.
FT   DISULFID       23     88
FT   STRAND          4      7
FT   STRAND         10     13
FT   TURN           15     16
FT   STRAND         19     25
FT   TURN           30     31
FT   STRAND         33     38
FT   TURN           40     41
FT   STRAND         44     49
FT   TURN           50     52
FT   STRAND         53     54
FT   TURN           56     57
FT   TURN           60     61
FT   STRAND         62     67
FT   TURN           68     69
FT   STRAND         70     75
FT   HELIX          80     82
FT   STRAND         85     90
FT   STRAND         97     98
FT   STRAND        102    106
FT   NON_TER       108    108
SQ   SEQUENCE   108 AA;  11902 MW;  9E8143E1188BCE2A CRC64;

  Query Match             9.2%;  Score 10;  DB 1;  Length 108;
  Best Local Similarity   100.0%;  Pred. No. 0.0025;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          42 PGKAPKLLIY 51
               ||||||||||
Db          40 PGKAPKLLIY 49


RESULT 8
KV5Q_MOUSE
ID   KV5Q_MOUSE      STANDARD;      PRT;   108 AA.
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AC   P01650;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-V region VPC 61.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=79195288; PubMed=109517;
RA   Vrana M., Rudikoff S., Potter M.;
RT   "The structural basis of a hapten-inhibitable kappa-chain idiotype.";
RL   J. Immunol. 122:1905-1910(1979).
CC   -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM MYELOMA PROTEINS THAT
CC       BIND BETA(2-1)-FRUCTOFURANOSYL MOIETIES (INULIN).
DR   PIR; A92808; KVM961.
DR   HSSP; P80362; 1WTL.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region.
FT   DOMAIN        1     23      FRAMEWORK-1.
FT   DOMAIN       24     34      COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN       35     49      FRAMEWORK-2.
FT   DOMAIN       50     56      COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN       57     88      FRAMEWORK-3.
FT   DOMAIN       89     97      COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN       98    108      FRAMEWORK-4.
FT   DISULFID     23     88      BY SIMILARITY.
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11809 MW;  FAE4DA36076F2AFE CRC64;

  Query Match          9.2%;  Score 10;  DB 1;  Length 108;
  Best Local Similarity  100.0%;  Pred. No. 0.0025;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          42 PGKAPKLLIY 51
               ||||||||||
Db          40 PGKAPKLLIY 49


RESULT 9
KV5R_MOUSE
ID   KV5R_MOUSE      STANDARD;      PRT;   108 AA.
AC   P01651;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-V region EPC 109.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=79195288; PubMed=109517;
RA   Vrana M., Rudikoff S., Potter M.;
RT   "The structural basis of a hapten-inhibitable kappa-chain idiotype.";
RL   J. Immunol. 122:1905-1910(1979).
CC   -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM MYELOMA PROTEINS THAT
CC       BIND BETA(2-1)-FRUCTOFURANOSYL MOIETIES (INULIN).
DR   PIR; B92808; KVM809.
DR   HSSP; P01607; 1REI.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region.
FT   DOMAIN        1     23      FRAMEWORK-1.
FT   DOMAIN       24     34      COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN       35     49      FRAMEWORK-2.
FT   DOMAIN       50     56      COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN       57     88      FRAMEWORK-3.
FT   DOMAIN       89     97      COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN       98    108      FRAMEWORK-4.
FT   DISULFID     23     88      BY SIMILARITY.
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11810 MW;  8DE4DD31076F2AFB CRC64;

  Query Match          9.2%;  Score 10;  DB 1;  Length 108;
  Best Local Similarity  100.0%;  Pred. No. 0.0025;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          42 PGKAPKLLIY 51
               ||||||||||
Db          40 PGKAPKLLIY 49


RESULT 10
KV5S_MOUSE
ID   KV5S_MOUSE      STANDARD;      PRT;   108 AA.
AC   P01652;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-V region J606.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=82099361; PubMed=6798111;
RA   Johnson N., Slankard J., Paul L., Hood L.;
RT   "The complete V domain amino acid sequences of two myeloma inulin-
RT   binding proteins.";
RL   J. Immunol. 128:302-307(1982).
CC   -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM MYELOMA PROTEINS THAT
CC       BIND BETA(2-1)-FRUCTOFURANOSYL MOIETIES (INULIN).
DR   PIR; A92811; KVM806.
DR   HSSP; P01607; 1REI.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region.
FT   DOMAIN        1     23      FRAMEWORK-1.
FT   DOMAIN       24     34      COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN       35     49      FRAMEWORK-2.
FT   DOMAIN       50     56      COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN       57     88      FRAMEWORK-3.
FT   DOMAIN       89     97      COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN       98    108      FRAMEWORK-4.
FT   DISULFID     23     88      BY SIMILARITY.
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11810 MW;  8DE4DD31076F2AFB CRC64;

  Query Match          9.2%;  Score 10;  DB 1;  Length 108;
  Best Local Similarity  100.0%;  Pred. No. 0.0025;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          42 PGKAPKLLIY 51
               ||||||||||
Db          40 PGKAPKLLIY 49


RESULT 11
KV5T_MOUSE
ID   KV5T_MOUSE      STANDARD;      PRT;   108 AA.
AC   P01653;
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DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-V region W3082.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=82099361; PubMed=6798111;
RA   Johnson M., Blankard J., Paul L., Hood L.;
RT   "The complete V domain amino acid sequences of two myeloma inulin-
RT   binding proteins.";
RL   J. Immunol. 128:302-307(1982).
CC   -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM MYELOMA PROTEINS THAT
CC       BIND BETA(2-1)-FRUCTOFURANOSYL MOIETIES (INULIN).
DR   PIR; B92811; KVMSB2.
DR   HSSP; P80362; 1WTL.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region.
FT   DOMAIN      1     23       FRAMEWORK-1.
FT   DOMAIN     24     34       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN     35     49       FRAMEWORK-2.
FT   DOMAIN     50     56       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN     57     88       FRAMEWORK-3.
FT   DOMAIN     89     97       COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN     98    108       FRAMEWORK-4.
FT   DISULFID   23     88       BY SIMILARITY.
FT   NON_TER   108    108
SQ   SEQUENCE   108 AA;  11850 MW;  C5C145DC376F30CD CRC64;

  Query Match          9.2%;  Score 10;  DB 1;  Length 108;
  Best Local Similarity  100.0%;  Pred. No. 0.0025;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          42 PGKAPKLLIY 51
               ||||||||||
Db          40 PGKAPKLLIY 49


RESULT 12
LV3A_HUMAN
ID   LV3A_HUMAN     STANDARD;      PRT;   108 AA.
AC   P01714;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Ig lambda chain V-III region SH.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=70166723; PubMed=4909564;
RA   Titani K., Wikler M., Shinoda T., Putnam F.W.;
RT   "The amino acid sequence of a lambda type Bence-Jones protein. 3. The
RT   complete amino acid sequence and the location of the disulfide
RT   bridges.";
RL   J. Biol. Chem. 245:2171-2176(1970).
CC   -!- MISCELLANEOUS: This is a Bence-Jones protein.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR   PIR; A01980; L3HUSH.
DR   HSSP; P80748; 2LOI.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Bence-Jones protein.
FT   DOMAIN      1     23       FRAMEWORK-1.
FT   DOMAIN     24     34       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN     35     49       FRAMEWORK-2.
FT   DOMAIN     50     56       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN     57     88       FRAMEWORK-3.
FT   DOMAIN     89     97       COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN     98    107       FRAMEWORK-4.
FT   DISULFID   23     88       BY SIMILARITY.
FT   NON_TER   108    108
SQ   SEQUENCE   108 AA;  11292 MW;  E7E122958641A56 CRC64;

  Query Match          9.2%;  Score 10;  DB 1;  Length 108;
  Best Local Similarity  100.0%;  Pred. No. 0.0025;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          81 QAEDEADYYC 90
               ||||||||||
Db          77 QAEDEADYYC 86


RESULT 13
KVLS_HUMAN
ID   KVLS_HUMAN     STANDARD;      PRT;   108 AA.
AC   P01611;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-I region Wes.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=81092279; PubMed=6778806;
RA   Kratzin H., Yang C., Krusche U., Hilschmann N.;
RT   "Preparative separation of the tryptic hydrolysate of a protein by
RT   high-pressure liquid chromatography. The primary structure of a
RT   monoclonal L-chain of k-type, subgroup I (Bence-Jones Protein
RT   Wes).";
RL   Hoppe-Seyler's Z. Physiol. Chem. 361:1591-1598(1980).
CC   -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC   -!- MISCELLANEOUS: This is a Bence-Jones protein.
DR   PIR; A01877; K1HUWS.
DR   HSSP; P80362; 1WTL.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Bence-Jones protein.
FT   DOMAIN      1     23       FRAMEWORK-1.
FT   DOMAIN     24     34       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN     35     49       FRAMEWORK-2.
FT   DOMAIN     50     56       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN     57     88       FRAMEWORK-3.
FT   DOMAIN     89     97       COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN     98    107       FRAMEWORK-4.
FT   DISULFID   23     88       BY SIMILARITY.
FT   NON_TER   108    108
SQ   SEQUENCE   108 AA;  11608 MW;  782B14A649A60E45 CRC64;

  Query Match          8.3%;  Score 9;  DB 1;  Length 108;
  Best Local Similarity  100.0%;  Pred. No. 0.029;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          43 GKAPKLLIY 51
               |||||||||
Db          41 GKAPKLLIY 49
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RESULT 14
KV1T_HUMAN
ID   KV1T_HUMAN      STANDARD;      PRT;   109 AA.
AC   P01612;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Ig kappa chain V-I region Mev.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=83081018; PubMed=6816713;
RA   Eulitz M., Linke R.P.;
RT   "Primary structure of the variable part of an amyloidogenic
RT   Bence-Jones Protein (Mev). An unusual insertion in the third
RT   hypervariable region of a human kappa-immunoglobulin light chain.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 363:1347-1358(1982).
CC   -!- MISCELLANEOUS: ANOTHER FORM THAT LACKED RESIDUES 1-3 WAS ALSO
CC       FOUND.
CC   -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
DR   PIR; A01879; KIHUMV.
DR   HSSP; P80362; 1WTL.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGV; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Bence-Jones protein.
FT   DOMAIN      1     23       FRAMEWORK-1.
FT   DOMAIN     24     34       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN     35     49       FRAMEWORK-2.
FT   DOMAIN     50     56       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN     57     88       FRAMEWORK-3.
FT   DOMAIN     89     98       COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN     99    108       FRAMEWORK-4.
FT   DISULFID   23     88       BY SIMILARITY.
FT   NON_TER   108    108
SQ   SEQUENCE   108 AA;  11870 MW;  B6ABF4515D55F5A0 CRC64;

  Query Match          8.3%;  Score 9;  DB 1;  Length 109;
  Best Local Similarity   100.0%;  Pred. No. 0.03;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          42 PGKAPKLLI 50
               |||||||||
Db          40 PGKAPKLLI 48


RESULT 15
KV1F_HUMAN
ID   KV1F_HUMAN      STANDARD;      PRT;   108 AA.
AC   P01598;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-I region EU.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=71064023; PubMed=5489770;
RA   Gottlieb P.D., Cunningham B.A., Rutishauser U., Edelman G.M.;
RT   "The covalent structure of a human gamma G-immunoglobulin. VI. Amino
RT   acid sequence of the light chain.";
RL   Biochemistry 9:3155-3161(1970).

RN   [2]
RP   DISULFIDE BOND.
RX   MEDLINE=71064027; PubMed=4923144;
RA   Gall W.E., Edelman G.M.;
RT   "The covalent structure of a human gamma G-immunoglobulin. X.
RT   Intrachain disulfide bonds.";
RL   Biochemistry 9:3188-3196(1970).
CC   -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC   -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
DR   PIR; A90562; KIHUSU.
DR   HSSP; P01607; 1REI.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGV; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region.
FT   DOMAIN      1     23       FRAMEWORK-1.
FT   DOMAIN     24     34       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN     35     49       FRAMEWORK-2.
FT   DOMAIN     50     56       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN     57     88       FRAMEWORK-3.
FT   DOMAIN     89     97       COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN     98    107       FRAMEWORK-4.
FT   DISULFID   23     88
FT   NON_TER   108    108
SQ   SEQUENCE   108 AA;  11788 MW;  9CD294F2F4D88823 CRC64;

  Query Match          7.3%;  Score 9;  DB 1;  Length 108;
  Best Local Similarity   100.0%;  Pred. No. 0.34;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          42 PGKAPKLL 49
               ||||||||
Db          40 PGKAPKLL 47


RESULT 16
KV1L_HUMAN
ID   KV1L_HUMAN      STANDARD;      PRT;   108 AA.
AC   P01604;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-I region Kue.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=79237924; PubMed=112021;
RA   Eulitz M., Kley H.-P., Zeitler H.-J.;
RT   "The primary structure of the Bence-Jones protein Kue. The amino acid
RT   sequence of the variable part of a human L-chain of the kappa-type.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 360:725-734(1979).
CC   -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC   -!- MISCELLANEOUS: This is a Bence-Jones protein.
DR   PIR; A01870; KIHUKU.
DR   HSSP; P01607; 1REI.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGV; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Bence-Jones protein.
FT   DOMAIN      1     23       FRAMEWORK-1.
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FT   DOMAIN        24      34       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN        35      49       FRAMEWORK-2.
FT   DOMAIN        50      56       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN        57      88       FRAMEWORK-3.
FT   DOMAIN        89      97       COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN        98     107       FRAMEWORK-4
FT   DISULFID      23      88       BY SIMILARITY.
FT   NON_TER      108     108
SQ   SEQUENCE   108 AA;  12127 MW;  906679A5D90E4E98 CRC64;

  Query Match             7.3%;  Score 8;  DB 1;  Length 108;
  Best Local Similarity   100.0%;  Pred. No. 0.34;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          44 KAPKLLIY 51
               ||||||||
Db          42 KAPKLLIY 49


RESULT 17
LV1F_HUMAN
ID   LV1F_HUMAN      STANDARD;      PRT;   109 AA.
AC   P04208;
DT   20-MAR-1987 (Rel. 04, Created)
DT   20-MAR-1987 (Rel. 04, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig lambda chain V-I region WAH.
OS   Homo sapiens (Human)
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=83221661; PubMed=6407018;
RA   Takahashi Y., Takahashi N., Tetaert D., Putnam F.W.;
RT   "Complete covalent structure of a human immunoglobulin D: sequence of
RT   the lambda light chain.";
RL   Proc. Natl. Acad. Sci. U.S.A. 80:3686-3690(1983).
DR   PIR; A01967; L1HUWA.
DR   HSSP; P01703; 7FAB.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_V.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGV; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region.
FT   DOMAIN        1      97       V SEGMENT.
FT   DOMAIN       98     109       J SEGMENT.
FT   DISULFID     22      89       BY SIMILARITY.
FT   NON_TER     109     109
SQ   SEQUENCE   109 AA;  11725 MW;  B17785F6A8DF9BAC CRC64;

  Query Match             7.3%;  Score 8;  DB 1;  Length 109;
  Best Local Similarity   100.0%;  Pred. No. 0.34;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          63 RFSGSKSG 70
               ||||||||
Db          62 RFSGSKSG 69


RESULT 18
LV1I_HUMAN
ID   LV1I_HUMAN      STANDARD;      PRT;   109 AA.
AC   P06685;
DT   01-JAN-1988 (Rel. 06, Created)
DT   01-JAN-1988 (Rel. 06, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Ig lambda chain V-I region EPS.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=86000126; PubMed=3929803;
RA   Toft K.G., Sletten K., Husby G.;
RT   "The amino-acid sequence of the variable region of a carbohydrate-
RT   containing amyloid fibril protein EPS (immunoglobulin light chain,
RT   type lambda).";
RL   Biol. Chem. Hoppe-Seyler 366:617-625(1985).
CC   -!- MISCELLANEOUS: RESIDUES 1-2, 56-62, AND 74-78 AND THE SEQUENCED
CC       PEPTIDES WERE POSITIONED BY HOMOLOGY.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR   PIR; A24656; L1HUEP.
DR   HSSP; P01703; 7FAB.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_V.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGV; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Amyloid; Glycoprotein.
FT   DOMAIN        1     105       IG-LIKE.
FT   CARBOHYD    104     104       N-LINKED (GLCNAC. . .).
FT   DISULFID     22      89       BY SIMILARITY.
FT   NON_TER     109     109
SQ   SEQUENCE   109 AA;  11414 MW;  556A313B24D5AC73 CRC64;

  Query Match             7.3%;  Score 8;  DB 1;  Length 109;
  Best Local Similarity   100.0%;  Pred. No. 0.34;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          63 RFSGSKSG 70
               ||||||||
Db          62 RFSGSKSG 69


RESULT 19
KV1I_RABIT
ID   KV1I_RABIT      STANDARD;      PRT;    94 AA.
AC   P01692;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa-B5 chain V region 2699 (Fragments).
OS   Oryctolagus cuniculus (Rabbit)
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=83178897; PubMed=6404296;
RA   Ayadi H., Dutka S., Paroutaud P., Strosberg A.D.;
RT   "Partial amino acid sequence of a rabbit immunoglobulin light chain
RT   of allotype b5.";
RL   Biochemistry 22:993-998(1983).
CC   -!- MISCELLANEOUS: THIS CHAIN IS AN ANTIBODY TO PNEUMOCOCCUS STRAIN
CC       III VACCINE.
DR   PIR; A01955; A01955.
DR   HSSP; P01607; 1REI.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003599; Ig.
DR   SMART; SM00409; IG; 1.
KW   Immunoglobulin V region.
FT   DOMAIN        1      23       FRAMEWORK-1.
FT   DOMAIN       24      34       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN       35      49       FRAMEWORK-2.
FT   DOMAIN       50      56       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN       57     >82       FRAMEWORK-3.
FT   NON_CONS     82      83
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FT   DOMAIN      <83      83        COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN       84      93        FRAMEWORK-4.
FT   VARIANT       8       8        P -> A.
FT   VARIANT      22      22        N -> K.
FT   NON_TER      94      94
SQ   SEQUENCE   94 AA;  9469 MW;  351D977B93252EBC CRC64;

  Query Match             6.4%;  Score 7;  DB 1;  Length 94;
  Best Local Similarity   100.0%;  Pred. No. 3.5;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          100 FGGGTKV 106
                |||||||
Db           84 FGGGTKV 90


RESULT 20
LV4A_HUMAN
ID   LV4A_HUMAN      STANDARD;      PRT;   106 AA.
AC   P01715;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Ig lambda chain V-IV region Bau.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=75059189; PubMed=4435717;
RA   Baczko K., Braun D., Hilschmann N.;
RT   "Patterns of antibody structure, the primary structure of monoclonal
RT   immunoglobulin L-chain of the lambda-type, subgroup IV (Bence-Jones
RT   protein Bau).";
RL   Hoppe-Seyler's Z. Physiol. Chem. 355:131-154(1974).
CC   -!- MISCELLANEOUS: This is a Bence-Jones protein.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR   PIR; A01981; L4HUBU.
DR   HSSP; P80748; 2LOI.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Bence-Jones protein.
FT   DOMAIN       1    102        IG-LIKE.
FT   NON_TER    106    106
SQ   SEQUENCE   106 AA;  11305 MW;  4B6A688E0EC46571 CRC64;

  Query Match             6.4%;  Score 7;  DB 1;  Length 106;
  Best Local Similarity   100.0%;  Pred. No. 3.9;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy           84 DEADYVC 90
                |||||||
Db           80 DEADYVC 86


RESULT 21
LV4B_HUMAN
ID   LV4B_HUMAN      STANDARD;      PRT;   106 AA.
AC   P01716;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Ig lambda chain V-IV region X.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=69088380; PubMed=4883841;
RA   Milstein C., Clegg J.B., Jarvis J.M.;
RT   "Immunoglobulin lambda-chains. The complete amino acid sequence of a
RT   Bence-Jones protein.";
RL   Biochem. J. 110:631-652(1968).
CC   -!- MISCELLANEOUS: This is a Bence-Jones protein.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR   PIR; A01982; L4HUX.
DR   HSSP; P80748; 2LOI.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Bence-Jones protein.
FT   DOMAIN       1    102        IG-LIKE.
FT   NON_TER    106    106
SQ   SEQUENCE   106 AA;  11334 MW;  24D04344AA812855 CRC64;

  Query Match             6.4%;  Score 7;  DB 1;  Length 106;
  Best Local Similarity   100.0%;  Pred. No. 3.9;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy           84 DEADYVC 90
                |||||||
Db           80 DEADYVC 86


RESULT 22
LV4E_HUMAN
ID   LV4E_HUMAN      STANDARD;      PRT;   106 AA.
AC   P06889;
DT   01-JAN-1988 (Rel. 06, Created)
DT   01-JAN-1988 (Rel. 06, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Ig lambda chain V-IV region MOL.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=87156515; PubMed=3103603;
RA   Holm E., Sletten K., Husby G.;
RT   "Structural studies of a carbohydrate-containing
RT   immunoglobulin-lambda-light-chain amyloid-fibril protein (AL) of
RT   variable subgroup III.";
RL   Biochem. J. 239:545-551(1986).
CC   -!- MISCELLANEOUS: RESIDUES 29-30 AND 56-58 WERE POSITIONED BY
CC       HOMOLOGY.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR   PIR; A26019; L4HUML.
DR   HSSP; P80748; 2LOI.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Amyloid; Glycoprotein.
FT   DOMAIN       1    103        IG-LIKE.
FT   DISULFID    21     86        BY SIMILARITY.
FT   CARBOHYD    90     90        N-LINKED (GLCNAC. . .) (PROBABLE).
FT   NON_TER    106    106
SQ   SEQUENCE   106 AA;  11272 MW;  D9BB77D4797D2123 CRC64;
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  Query Match             6.4%;  Score 7;  DB 1;  Length 106;
  Best Local Similarity   100.0%;  Pred. No. 3.9;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          84 DEADYYC 90
               |||||||
Db          80 DEADYYC 86


RESULT 23
KV1M_HUMAN
ID   KV1M_HUMAN      STANDARD;      PRT;   108 AA.
AC   P01605;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-I region Lay.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=77038198; PubMed=824717;
RA   Capra J.D., Klapper D.G.;
RT   "Complete amino acid sequence of the variable domains of two human
RT   IgM anti-gamma globulins (Lay/Pon) with shared idiotypic
RT   specificities.";
RL   Scand. J. Immunol. 5:677-684(1976).
CC   -!- MISCELLANEOUS: THE SECOND AND THIRD HYPERVARIABLE REGIONS OF THIS
CC       CHAIN ARE IDENTICAL WITH THOSE OF THE HUMAN POM V-III KAPPA CHAIN,
CC       WITH WHICH IT SHARES CERTAIN IDIOTYPIC DETERMINANTS.
CC   -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
CC       GLOBULIN ACTIVITY.
DR   PIR; A01871; KIHULY.
DR   HSSP; P01607; 1REI.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region.
FT   DOMAIN      1     23       FRAMEWORK-1.
FT   DOMAIN      24    34       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN      35    49       FRAMEWORK-2.
FT   DOMAIN      50    56       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN      57    88       FRAMEWORK-3.
FT   DOMAIN      89    97       COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN      98    107      FRAMEWORK-4.
FT   DISULFID    23    88       BY SIMILARITY.
FT   NON_TER     108   108
SQ   SEQUENCE   108 AA;  11834 MW;  739993A95431434A CRC64;

  Query Match             6.4%;  Score 7;  DB 1;  Length 108;
  Best Local Similarity   100.0%;  Pred. No. 4;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          45 APKLLIY 51
               |||||||
Db          43 APKLLIY 49


RESULT 24
KV1Y_HUMAN
ID   KV1Y_HUMAN      STANDARD;      PRT;   108 AA.
AC   P80362;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Ig kappa chain V-I region WAT.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE, AND X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX   MEDLINE=95086080; PubMed=7993911;
RA   Huang D.-B., Chang C.-H., Ainsworth C., Bruenger A.T., Bulitz M.,
RA   Solomon A., Stevens F.J., Schiffer M.;
RT   "Comparison of crystal structures of two homologous proteins:
RT   structural origin of altered domain interactions in immunoglobulin
RT   light-chain dimers.";
RL   Biochemistry 33:14848-14857(1994).
RN   [2]
RP   SEQUENCE OF 1-35.
RX   MEDLINE=81267384; PubMed=6167731;
RA   Stevens F.J., Westholm F.A., Panagiotopoulos N., Schiffer M.,
RA   Popp R.A., Solomon A.;
RT   "Characterization and preliminary crystallographic data on the VL-
RT   related fragment of the human KI Bence Jones protein WAT.";
RL   J. Mol. Biol. 147:185-193(1981).
CC   -!- MISCELLANEOUS: This is a Bence-Jones protein.
DR   PDB; 1WTL; 01-NOV-94.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_V.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Bence-Jones protein; 3D-structure.
FT   DOMAIN      1     23       FRAMEWORK-1.
FT   DOMAIN      24    34       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN      35    49       FRAMEWORK-2.
FT   DOMAIN      50    56       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN      57    88       FRAMEWORK-3.
FT   DOMAIN      89    97       COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN      98    107      FRAMEWORK-4.
FT   DISULFID    23    88       BY SIMILARITY.
FT   CONFLICT    30    31       TN -> SD (IN REF. 2).
FT   STRAND      4     7
FT   STRAND      10    13
FT   TURN        15    16
FT   STRAND      19    25
FT   TURN        30    31
FT   STRAND      33    38
FT   TURN        40    41
FT   STRAND      45    49
FT   TURN        50    52
FT   STRAND      53    54
FT   TURN        56    57
FT   TURN        60    61
FT   STRAND      62    67
FT   TURN        68    69
FT   STRAND      70    75
FT   HELIX       80    82
FT   STRAND      84    90
FT   STRAND      98    98
FT   STRAND      102   106
FT   NON_TER     108   108
SQ   SEQUENCE   108 AA;  11737 MW;  D9D941B3F0FAE697 CRC64;

  Query Match             6.4%;  Score 7;  DB 1;  Length 108;
  Best Local Similarity   100.0%;  Pred. No. 4;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         100 PGGGTKV 106
               |||||||
Db          98 PGGGTKV 104
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RESULT 25
LV5A_HUMAN
ID   LV5A_HUMAN      STANDARD;      PRT;   108 AA.
AC   P01719;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Ig lambda chain V-V region DEL.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=75112179; PubMed=4452363;
RA   Eulitz M.;
RT   "A new subgroup of human L-chains of the lambda-type. Primary
RT   structure of Bence-Jones protein DEL.";
RL   Eur. J. Biochem. 50:49-69(1974).
CC   -!- MISCELLANEOUS: THIS IS THE FIRST SEQUENCED V REGION OF LAMBDA
CC       CHAIN SUBGROUP V.
CC   -!- MISCELLANEOUS: This is a Bence-Jones protein.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR   PIR; A01985; LSHUDL.
DR   HSSP; P80748; 2LOI.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Bence-Jones protein.
FT   DOMAIN        1     97       IG-LIKE.
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11342 MW;  B8E8ED9C09C9E451 CRC64;

  Query Match              6.4%;  Score 7;  DB 1;  Length 108;
  Best Local Similarity   100.0%;  Pred. No. 4;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         84 DEADYYC 90
              |||||||
Db         80 DEADYYC 86


Search completed: March 15, 2004, 07:42:33
Job time : 19 secs
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